

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 29, 2001, 13:49:17 ; Search time 172.16 Seconds  
(without alignments)  
746.106 Million cell updates/sec

Title: US-09-466-396A-176  
Perfect score: 2956  
Sequence: 1 MNKLYIGNLSENAAPSDLES.....VKHQOQKALQSGPPQSRRK 579

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2803329 seqs, 221847457 residues

Total number of hits satisfying chosen parameters: 2803329

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main.\*

- 1: /cgn2\_6/ptodata/2/paa/PCRTUS\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/paa/US06\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/paa/US080\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/paa/US081\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/paa/US082\_COMB.pep.\*
- 7: /cgn2\_6/ptodata/2/paa/US083\_COMB.pep.\*
- 8: /cgn2\_6/ptodata/2/paa/US084\_COMB.pep.\*
- 9: /cgn2\_6/ptodata/2/paa/US085\_COMB.pep.\*
- 10: /cgn2\_6/ptodata/2/paa/US086\_COMB.pep.\*
- 11: /cgn2\_6/ptodata/2/paa/US087\_COMB.pep.\*
- 12: /cgn2\_6/ptodata/2/paa/US088\_COMB.pep.\*
- 13: /cgn2\_6/ptodata/2/paa/US089\_COMB.pep.\*
- 14: /cgn2\_6/ptodata/2/paa/US090\_COMB.pep.\*
- 15: /cgn2\_6/ptodata/2/paa/US091\_COMB.pep.\*
- 16: /cgn2\_6/ptodata/2/paa/US092\_COMB.pep.\*
- 17: /cgn2\_6/ptodata/2/paa/US093\_COMB.pep.\*
- 18: /cgn2\_6/ptodata/2/paa/US094\_COMB.pep.\*
- 19: /cgn2\_6/ptodata/2/paa/US095\_COMB.pep.\*
- 20: /cgn2\_6/ptodata/2/paa/US096\_COMB.pep.\*
- 21: /cgn2\_6/ptodata/2/paa/US097\_COMB.pep.\*
- 22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep.\*
- 23: /cgn2\_6/ptodata/2/paa/US099\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2956	100.0	579	18	US-09-466-396A-176
2	2956	100.0	579	19	US-09-542-615A-176
3	2956	100.0	579	20	US-09-606-421A-176
4	2956	100.0	579	20	US-09-630-940A-176
5	2956	100.0	579	20	US-09-643-597-176
6	2956	100.0	579	20	US-09-662-786-176
7	2956	100.0	579	20	US-09-685-696-176
8	2956	100.0	579	21	US-09-735-705-176
9	2956	100.0	579	22	US-09-850-176-176
10	2956	100.0	579	22	US-09-850-176-176

11	2943	99.6	579	19	US-09-542-615A-348	Sequence 348, App
12	2943	99.6	579	20	US-09-606-421A-348	Sequence 348, App
13	2943	99.6	579	20	US-09-630-940A-348	Sequence 348, App
14	2943	99.6	579	20	US-09-630-940B-348	Sequence 348, App
15	2943	99.6	579	20	US-09-643-597-348	Sequence 348, App
16	2943	99.6	579	20	US-09-662-786-348	Sequence 348, App
17	2943	99.6	579	20	US-09-685-696-348	Sequence 348, App
18	2943	99.6	579	21	US-09-735-705-348	Sequence 348, App
19	2943	99.6	579	22	US-09-850-716-348	Sequence 348, App
20	2938	99.4	586	22	US-09-850-716-427	Sequence 427, App
21	1950.5	66.0	603	1	PCT-US01-01307-592	Sequence 592, App
22	1946.5	65.8	620	1	PCT-US01-01341-1116	Sequence 1116, App
23	949	32.1	261	1	PCT-US01-01341-1114	Sequence 1114, App
24	919	31.1	250	1	PCT-US01-01341-1532	Sequence 1532, App
25	896	30.3	1219	23	US-60-161-932-1355	Sequence 1355, App
26	835.5	28.3	558	23	US-60-191-637-1899	Sequence 1899, App
27	835.5	28.3	558	23	US-60-191-681-1524	Sequence 1524, App
28	832.5	28.2	558	23	US-60-167-217-1955	Sequence 1955, App
29	832.5	28.2	558	23	US-60-173-464-1602	Sequence 1602, App
30	626	21.2	171	1	PCT-US01-01341-1119	Sequence 1119, App
31	527	17.8	192	1	PCT-US01-01341-1117	Sequence 1117, App
32	503.5	17.0	136	23	US-60-236-804-688	Sequence 688, App
33	474	16.0	93	1	PCT-US01-00663-38770	Sequence 38770, App
34	437	14.8	144	23	US-60-188-162-2591	Sequence 2591, App
35	402	13.6	171	1	PCT-US01-01341-1536	Sequence 1536, App
36	360.5	12.2	131	1	PCT-US01-01307-848	Sequence 848, App
37	282	9.5	182	23	US-60-146-394-1584	Sequence 1584, App
38	280	9.5	182	23	US-60-143-992-1350	Sequence 1350, App
39	229	7.7	386	23	US-60-167-217-16663	Sequence 16663, App
40	229	7.7	386	23	US-60-173-464-13643	Sequence 13643, App
41	229	7.7	386	23	US-60-191-637-16673	Sequence 16673, App
42	229	7.7	386	23	US-60-191-681-13184	Sequence 13184, App
43	227	7.7	45	1	PCT-US01-00663-37584	Sequence 37584, App
44	226	7.6	1268	23	US-60-167-216-264	Sequence 264, App
45	226	7.6	1268	23	US-60-173-464-8713	Sequence 8713, App

ALIGNMENTS

RESULT 1  
US-09-466-396A-176  
; Sequence 176, Application US/09466396A  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C4  
; CURRENT APPLICATION NUMBER: US/09/466,396A  
; CURRENT FILING DATE: 1999-12-17  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 176  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-466-396A-176

Query Match 100.0%; Score 2956; DB 18; Length 579;  
Best Local Similarity 100.0%; Pred. No. 2.8e-243;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNKLTYGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGVAFDPCDSEWALKAIALSGK	60
Db	1	MNKLTYGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGVAFDPCDSEWALKAIALSGK	60
Qy	61	IELHGKPIEVEHSVPKQRIRKLIQIRNIPPHLQWEVLDLSLLVQYGVVSECEQVNTDSETA	120
Db	61	IELHGKPIEVEHSVPKQRIRKLIQIRNIPPHLQWEVLDLSLLVQYGVVSECEQVNTDSETA	120
Qy	121	VYNYTSSKQARQALDKUNGFOLENTFKVAYIPDEMAAQNPLQOPRRGLGORGSS	180
		Sequence 176, App	

Db 121 VVNTYSSKQARQALDKLNGFLENFTLVKVAIPDEMAAQNPLQQRGRRLGQRSS 180  
Qy 181 ROGSPGSVSKQPCDPLRLLLVPTQFVGAIIKKEGATIRNITKOTQSKIDVHRKENAGAA 240  
Db 181 ROGSPGSVSKQPCDPLRLLLVPTQFVGAIIKKEGATIRNITKOTQSKIDVHRKENAGAA 240  
Qy 241 EKSTIILSTPGTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRILIGKEGRNLK 300  
Db 241 EKSTIILSTPGTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRILIGKEGRNLK 300  
Qy 301 KIEQDQTKITISPLQELTYLNPRTITVKGNETVETCAKAEIEIMKKIRESYENDIASNNL 360  
Db 301 KIEQDQTKITISPLQELTYLNPRTITVKGNETVETCAKAEIEIMKKIRESYENDIASNNL 360  
Qy 361 QAHILPGLNLAGLFPPTSGMPPTSGPPSAMPPTPPQFQSETETVHQIPALSVCAGI 420  
Db 361 QAHILPGLNLAGLFPPTSGMPPTSGPPSAMPPTPPQFQSETETVHQIPALSVCAGI 420  
Qy 421 IKGOGHITKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQGRYIKKEENFV 480  
Db 421 IKGOGHITKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQGRYIKKEENFV 480  
Qy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNLQNLSSAEVVVPRDQTPDENDQVVVKIT 540  
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNLQNLSSAEVVVPRDQTPDENDQVVVKIT 540  
Qy 541 GHFYACQVQAKRIQEIILTVKQHQOQKALQSGPPQSRK 579  
Db 541 GHFYACQVQAKRIQEIILTVKQHQOQKALQSGPPQSRK 579

## RESULT 2

US-09-542-615A-176  
; Sequence 176, Application US/09542615A  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy A.  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY  
; FILE REFERENCE: 210121.455C8  
; CURRENT APPLICATION NUMBER: US/09/542.615A  
; CURRENT FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 350  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 176  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-542-615A-176

Query Match 100.0%; Score 2956; DB 19; Length 579;  
Best Local Similarity 100.0%; Pred. No. 2.8e-243;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSNAAPSDESIFKDAKIPVSGPFLVKTGYAFVDCPDESQWALKATEALSGK 60  
Db 1 MNKLYIGNLSNAAPSDESIFKDAKIPVSGPFLVKTGYAFVDCPDESQWALKATEALSGK 60  
Qy 61 IELHGKPIEVSHSVKQRIRKLRINIPHLQWELVDSLLVQGVVESCQVNTDSETA 120  
Db 61 IELHGKPIEVSHSVKQRIRKLRINIPHLQWELVDSLLVQGVVESCQVNTDSETA 120  
Qy 121 VVNTYSSKQARQALDKLNGFLENFTLVKVAIPDEMAAQNPLQQRGRRLGQRSS 180  
Db 121 VVNTYSSKQARQALDKLNGFLENFTLVKVAIPDEMAAQNPLQQRGRRLGQRSS 180  
Qy 181 ROGSPGSVSKQPCDPLRLLLVPTQFVGAIIKKEGATIRNITKOTQSKIDVHRKENAGAA 240

Db 181 ROGSPGSVSKQPCDPLRLLLVPTQFVGAIIKKEGATIRNITKOTQSKIDVHRKENAGAA 240  
Qy 241 EKSTIILSTPGTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRILIGKEGRNLK 300  
Db 241 EKSTIILSTPGTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRILIGKEGRNLK 300  
Qy 301 KIEQDQTKITISPLQELTYLNPRTITVKGNETVETCAKAEIEIMKKIRESYENDIASNNL 360  
Db 301 KIEQDQTKITISPLQELTYLNPRTITVKGNETVETCAKAEIEIMKKIRESYENDIASNNL 360  
Qy 361 QAHILPGLNLAGLFPPTSGMPPTSGPPSAMPPTPPQFQSETETVHQIPALSVCAGI 420  
Db 361 QAHILPGLNLAGLFPPTSGMPPTSGPPSAMPPTPPQFQSETETVHQIPALSVCAGI 420  
Qy 421 IKGOGHITKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQGRYIKKEENFV 480  
Db 421 IKGOGHITKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQGRYIKKEENFV 480  
Qy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNLQNLSSAEVVVPRDQTPDENDQVVVKIT 540  
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNLQNLSSAEVVVPRDQTPDENDQVVVKIT 540  
Qy 541 GHFYACQVQAKRIQEIILTVKQHQOQKALQSGPPQSRK 579  
Db 541 GHFYACQVQAKRIQEIILTVKQHQOQKALQSGPPQSRK 579

## RESULT 3

US-09-606-421A-176  
; Sequence 176, Application US/09606421A  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C9  
; CURRENT APPLICATION NUMBER: US/09/606.421A  
; CURRENT FILING DATE: 2000-06-28  
; NUMBER OF SEQ ID NOS: 354  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 176  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-606-421A-176

Query Match 100.0%; Score 2956; DB 20; Length 579;  
Best Local Similarity 100.0%; Pred. No. 2.8e-243;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSNAAPSDESIFKDAKIPVSGPFLVKTGYAFVDCPDESQWALKATEALSGK 60  
Db 1 MNKLYIGNLSNAAPSDESIFKDAKIPVSGPFLVKTGYAFVDCPDESQWALKATEALSGK 60  
Qy 61 IELHGKPIEVSHSVKQRIRKLRINIPHLQWELVDSLLVQGVVESCQVNTDSETA 120  
Db 61 IELHGKPIEVSHSVKQRIRKLRINIPHLQWELVDSLLVQGVVESCQVNTDSETA 120  
Qy 121 VVNTYSSKQARQALDKLNGFLENFTLVKVAIPDEMAAQNPLQQRGRRLGQRSS 180  
Db 121 VVNTYSSKQARQALDKLNGFLENFTLVKVAIPDEMAAQNPLQQRGRRLGQRSS 180  
Qy 181 ROGSPGSVSKQPCDPLRLLLVPTQFVGAIIKKEGATIRNITKOTQSKIDVHRKENAGAA 240  
Db 181 ROGSPGSVSKQPCDPLRLLLVPTQFVGAIIKKEGATIRNITKOTQSKIDVHRKENAGAA 240



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Db 181 RQSPGVSQKPCDPLRLLLVPTQFVGAIIGKGGATIRNITKTQSKIDVHRKENAGAA 240
Qy 241 EKSTITLSTPGTSAACKSILEIMHKEAQDIKFTTEEPLKTLAHNNFVGRILIGEGRNK 300
Db 241 EKSTITLSTPGTSAACKSILEIMHKEAQDIKFTTEEPLKTLAHNNFVGRILIGEGRNK 300
Qy 301 KIEQDTTKITISPLQELTYLNPERTITVKNVETCAKAEIEIMKKIRESYENDIASNNL 360
Db 301 KIEQDTTKITISPLQELTYLNPERTITVKNVETCAKAEIEIMKKIRESYENDIASNNL 360
Qy 361 QAHILPGLNLAGLFPPTSGMPPTSGPPSAMPPTPPYQFQSETEVHQFIPALSVCAL 420
Db 361 QAHILPGLNLAGLFPPTSGMPPTSGPPSAMPPTPPYQFQSETEVHQFIPALSVCAL 420
Qy 421 IGKOGQHIKQLSRFAGASIKIAPAEADPAKVRMVIITGPPPEAQFKAQGRYIKKEENFV 480
Db 421 IGKOGQHIKQLSRFAGASIKIAPAEADPAKVRMVIITGPPPEAQFKAQGRYIKKEENFV 480
Qy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSAEVVVPRDQTPDENDQVVKIT 540
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSAEVVVPRDQTPDENDQVVKIT 540
Qy 541 GHFYACQVAQRKIQEILITQVKHQHQKALQSGPPQSRKK 579
Db 541 GHFYACQVAQRKIQEILITQVKHQHQKALQSGPPQSRKK 579
```

## RESULT 6

US-09-643-597-176

; Sequence 176, Application US/09643597

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Henderson, Robert A.

; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C11

; CURRENT APPLICATION NUMBER: US/09/643.597

; CURRENT FILING DATE: 2000-08-21

; NUMBER OF SEQ ID NOS: 369

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 176

; LENGTH: 579

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-643-597-176

```
Query Match 100.0%; Score 2956; DB 20; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.8e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 MNKLYIGNLSENAAPSDESIFDKAIPVSGPFLVKTYGAFVDCPDSESWALKAEALSGK 60
Db 1 MNKLYIGNLSENAAPSDESIFDKAIPVSGPFLVKTYGAFVDCPDSESWALKAEALSGK 60
Qy 61 IELHGKPIEVESHVPKQRIRKLRIRNIPHLQWEVLDSLLVQYGVVSECEQVNTDSETA 120
Db 61 IELHGKPIEVESHVPKQRIRKLRIRNIPHLQWEVLDSLLVQYGVVSECEQVNTDSETA 120
Qy 121 VVNVYSSKQDQARQALDKLNGFLENFTLKVAYIPDEMAAQONPLQOPRGRRLGQGRSS 180
Db 121 VVNVYSSKQDQARQALDKLNGFLENFTLKVAYIPDEMAAQONPLQOPRGRRLGQGRSS 180
```

```
Qy 181 RQSPGVSQKPCDPLRLLLVPTQFVGAIIGKGGATIRNITKTQSKIDVHRKENAGAA 240
Db 181 RQSPGVSQKPCDPLRLLLVPTQFVGAIIGKGGATIRNITKTQSKIDVHRKENAGAA 240
Qy 241 EKSTITLSTPGTSAACKSILEIMHKEAQDIKFTTEEPLKTLAHNNFVGRILIGEGRNK 300
Db 241 EKSTITLSTPGTSAACKSILEIMHKEAQDIKFTTEEPLKTLAHNNFVGRILIGEGRNK 300
Qy 301 KIEQDTTKITISPLQELTYLNPERTITVKNVETCAKAEIEIMKKIRESYENDIASNNL 360
Db 301 KIEQDTTKITISPLQELTYLNPERTITVKNVETCAKAEIEIMKKIRESYENDIASNNL 360
Qy 361 QAHILPGLNLAGLFPPTSGMPPTSGPPSAMPPTPPYQFQSETEVHQFIPALSVCAL 420
Db 361 QAHILPGLNLAGLFPPTSGMPPTSGPPSAMPPTPPYQFQSETEVHQFIPALSVCAL 420
Qy 421 IGKOGQHIKQLSRFAGASIKIAPAEADPAKVRMVIITGPPPEAQFKAQGRYIKKEENFV 480
Db 421 IGKOGQHIKQLSRFAGASIKIAPAEADPAKVRMVIITGPPPEAQFKAQGRYIKKEENFV 480
Qy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSAEVVVPRDQTPDENDQVVKIT 540
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSAEVVVPRDQTPDENDQVVKIT 540
Qy 541 GHFYACQVAQRKIQEILITQVKHQHQKALQSGPPQSRKK 579
Db 541 GHFYACQVAQRKIQEILITQVKHQHQKALQSGPPQSRKK 579
```

## RESULT 7

US-09-662-786-176

; Sequence 176, Application US/09662786

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Henderson, Robert A.

; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C12

; CURRENT APPLICATION NUMBER: US/09/662.786

; CURRENT FILING DATE: 2000-09-15

; NUMBER OF SEQ ID NOS: 381

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 176

; LENGTH: 579

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-662-786-176

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Query Match 100.0%; Score 2956; DB 20; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.8e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 MNKLYIGNLSENAAPSDESIFDKAIPVSGPFLVKTYGAFVDCPDSESWALKAEALSGK 60
Db 1 MNKLYIGNLSENAAPSDESIFDKAIPVSGPFLVKTYGAFVDCPDSESWALKAEALSGK 60
Qy 61 IELHGKPIEVESHVPKQRIRKLRIRNIPHLQWEVLDSLLVQYGVVSECEQVNTDSETA 120
Db 61 IELHGKPIEVESHVPKQRIRKLRIRNIPHLQWEVLDSLLVQYGVVSECEQVNTDSETA 120
Qy 121 VVNVYSSKQDQARQALDKLNGFLENFTLKVAYIPDEMAAQONPLQOPRGRRLGQGRSS 180
Db 121 VVNVYSSKQDQARQALDKLNGFLENFTLKVAYIPDEMAAQONPLQOPRGRRLGQGRSS 180
```



QY 181 ROGSPGSVSKQPCDPLRLLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240  
DB 181 ROGSPGSVSKQPCDPLRLLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240  
QY 241 EKSITILSTPETSAAKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300  
DB 241 EKSITILSTPETSAAKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300  
QY 301 KIEQDTRKTIISPLOELTYNPRTITVKGNVETCAKAEEMKKIRIESYENDIASMNL 360  
DB 301 KIEQDTRKTIISPLOELTYNPRTITVKGNVETCAKAEEMKKIRIESYENDIASMNL 360  
QY 361 QAHLIPGLNLNAGLFPPTSGMPPTSGPPSAMPPTPYQFQSESETVHQFIPALSUGAI 420  
DB 361 QAHLIPGLNLNAGLFPPTSGMPPTSGPPSAMPPTPYQFQSESETVHQFIPALSUGAI 420  
QY 421 IKGQOHKIQLSRFAGASIKIAPAEAPDAKVRMVTITGPPPEAQFKAQRIYKIKEENFV 480  
DB 421 IKGQOHKIQLSRFAGASIKIAPAEAPDAKVRMVTITGPPPEAQFKAQRIYKIKEENFV 480  
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDQVVVKIT 540  
DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDQVVVKIT 540  
QY 541 GHFYACQVAQRKIQELTQVKHQHQQKALQSGPPQSRRK 579  
DB 541 GHFYACQVAQRKIQELTQVKHQHQQKALQSGPPQSRRK 579

## RESULT 8

US-09-685-696-176  
; Sequence 176, Application US/09685696  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C13  
; CURRENT APPLICATION NUMBER: US/09/685,696  
; CURRENT FILING DATE: 2000-10-09  
; NUMBER OF SEQ ID NOS: 381  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 176  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-685-696-176

Query Match 100.0%; Score 2956; DB 20; Length 579;  
Best Local Similarity 100.0%; Pred. No. 2.8e-243;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIALSGK 60  
DB 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIALSGK 60  
QY 61 IELHGKPIEVEHSVPKRIKQIRKQIRNIPPHLQWEVLDLSLLVQYGVVWESCEQVNTDSETA 120  
DB 61 IELHGKPIEVEHSVPKRIKQIRKQIRNIPPHLQWEVLDLSLLVQYGVVWESCEQVNTDSETA 120  
QY 121 VVNVITYSSKDQARQALDKLNGFOLNFVLKVAIIPDEMAAQONPQQPRGRGLQORSS 180  
DB 121 VVNVITYSSKDQARQALDKLNGFOLNFVLKVAIIPDEMAAQONPQQPRGRGLQORSS 180

DB 121 VVNVITYSSKDQARQALDKLNGFOLNFVLKVAIIPDEMAAQONPQQPRGRGLQORSS 180  
QY 181 ROGSPGSVSKQPCDPLRLLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240  
DB 181 ROGSPGSVSKQPCDPLRLLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240  
QY 241 EKSITILSTPETSAAKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300  
DB 241 EKSITILSTPETSAAKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300  
QY 301 KIEQDTRKTIISPLOELTYNPRTITVKGNVETCAKAEEMKKIRIESYENDIASMNL 360  
DB 301 KIEQDTRKTIISPLOELTYNPRTITVKGNVETCAKAEEMKKIRIESYENDIASMNL 360  
QY 361 QAHLIPGLNLNAGLFPPTSGMPPTSGPPSAMPPTPYQFQSESETVHQFIPALSUGAI 420  
DB 361 QAHLIPGLNLNAGLFPPTSGMPPTSGPPSAMPPTPYQFQSESETVHQFIPALSUGAI 420  
QY 421 IKGQOHKIQLSRFAGASIKIAPAEAPDAKVRMVTITGPPPEAQFKAQRIYKIKEENFV 480  
DB 421 IKGQOHKIQLSRFAGASIKIAPAEAPDAKVRMVTITGPPPEAQFKAQRIYKIKEENFV 480  
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDQVVVKIT 540  
DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDQVVVKIT 540  
QY 541 GHFYACQVAQRKIQELTQVKHQHQQKALQSGPPQSRRK 579  
DB 541 GHFYACQVAQRKIQELTQVKHQHQQKALQSGPPQSRRK 579

## RESULT 9

US-09-735-705-176  
; Sequence 176, Application US/09735705  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C14  
; CURRENT APPLICATION NUMBER: US/09/735,705  
; CURRENT FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 419  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 176  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-735-705-176

Query Match 100.0%; Score 2956; DB 21; Length 579;  
Best Local Similarity 100.0%; Pred. No. 2.8e-243;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIALSGK 60  
DB 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIALSGK 60  
QY 61 IELHGKPIEVEHSVPKRIKQIRKQIRNIPPHLQWEVLDLSLLVQYGVVWESCEQVNTDSETA 120  
DB 61 IELHGKPIEVEHSVPKRIKQIRKQIRNIPPHLQWEVLDLSLLVQYGVVWESCEQVNTDSETA 120

```
QY 121 VVNTYSSKQARQALDKLNGFQLENFTLVKVAIPDEMAAQNPLQOPRRRGLGQRSS 180
DB 121 VVNTYSSKQARQALDKLNGFQLENFTLVKVAIPDEMAAQNPLQOPRRRGLGQRSS 180
QY 181 ROGSPGVSQKPCDPLRLLLVPTQFVCAIIGKEGATIRNITKQSKIDVHRKENAGAA 240
DB 181 ROGSPGVSQKPCDPLRLLLVPTQFVCAIIGKEGATIRNITKQSKIDVHRKENAGAA 240
QY 241 EKSTILSTPEGSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300
DB 241 EKSTILSTPEGSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300
QY 301 KIEODTQKITISPLQELTYLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASNNL 360
DB 301 KIEODTQKITISPLQELTYLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASNNL 360
QY 361 QAHLPGLNLAGLFPPTSGMPPTSGPPSAMPPTPPYQFEQSETETVHOQIPALSVAI 420
DB 361 QAHLPGLNLAGLFPPTSGMPPTSGPPSAMPPTPPYQFEQSETETVHOQIPALSVAI 420
QY 421 IGKQGHQIKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQGRYIKKEENFV 480
DB 421 IGKQGHQIKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQGRYIKKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNELQNLSSAEVVVPRDQTPDENQDVVVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNELQNLSSAEVVVPRDQTPDENQDVVVKIT 540
QY 541 GHFYACQVAQRKIQEILTVKHQHQKALQSGPPQSRKK 579
DB 541 GHFYACQVAQRKIQEILTVKHQHQKALQSGPPQSRKK 579
```

## RESULT 10

US-09-850-716-176

; Sequence 176, Application US/09850716

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Henderson, Robert A.

; APPLICANT: McNeill, Patricia D.

; APPLICANT: Fanger, Neil

; APPLICANT: Retter, Marc W.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE REFERENCE: 210121.455C15

; CURRENT APPLICATION NUMBER: US/09/850,716

; CURRENT FILING DATE: 2001-05-07

; NUMBER OF SEQ ID NOS: 440

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 176

; LENGTH: 579

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-850-716-176

```
Query Match 100.0%; Score 2956; DB 22; Length 579;
Best Local Similarity 100.0%; Pred. No. 2.8e-243;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MNKLYIGNLSENAAPSDLESIFDKAIPVSGPFLVKTYAFVDCPDSEWALKATEALSGK 60
DB 1 MNKLYIGNLSENAAPSDLESIFDKAIPVSGPFLVKTYAFVDCPDSEWALKATEALSGK 60
QY 61 IELHGKPIEVHSPKQRIRKLIQIRNIPHLQWEVLDSLQVGVVSCQVNTDSETA 120
```

```
DB 61 IELHGKPIEVHSPKQRIRKLIQIRNIPHLQWEVLDSLQVGVVSCQVNTDSETA 120
QY 121 VVNTYSSKQARQALDKLNGFQLENFTLVKVAIPDEMAAQNPLQOPRRRGLGQRSS 180
DB 121 VVNTYSSKQARQALDKLNGFQLENFTLVKVAIPDEMAAQNPLQOPRRRGLGQRSS 180
QY 181 ROGSPGVSQKPCDPLRLLLVPTQFVCAIIGKEGATIRNITKQSKIDVHRKENAGAA 240
DB 181 ROGSPGVSQKPCDPLRLLLVPTQFVCAIIGKEGATIRNITKQSKIDVHRKENAGAA 240
QY 241 EKSTILSTPEGSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300
DB 241 EKSTILSTPEGSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300
QY 301 KIEODTQKITISPLQELTYLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASNNL 360
DB 301 KIEODTQKITISPLQELTYLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASNNL 360
QY 361 QAHLPGLNLAGLFPPTSGMPPTSGPPSAMPPTPPYQFEQSETETVHOQIPALSVAI 420
DB 361 QAHLPGLNLAGLFPPTSGMPPTSGPPSAMPPTPPYQFEQSETETVHOQIPALSVAI 420
QY 421 IGKQGHQIKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQGRYIKKEENFV 480
DB 421 IGKQGHQIKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAQFKAQGRYIKKEENFV 480
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNELQNLSSAEVVVPRDQTPDENQDVVVKIT 540
DB 481 SPKEEVKLEAHIRVPSFAAGRVIGKGTVNELQNLSSAEVVVPRDQTPDENQDVVVKIT 540
QY 541 GHFYACQVAQRKIQEILTVKHQHQKALQSGPPQSRKK 579
DB 541 GHFYACQVAQRKIQEILTVKHQHQKALQSGPPQSRKK 579
```

## RESULT 11

US-09-542-615A-348

; Sequence 348, Application US/09542615A

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy A.

; APPLICANT: Fanger, Gary R.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY

; FILE REFERENCE: 210121.455C8

; CURRENT APPLICATION NUMBER: US/09/542,615A

; CURRENT FILING DATE: 2000-04-14

; NUMBER OF SEQ ID NOS: 350

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 348

; LENGTH: 579

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-542-615A-348

```
Query Match 99.6%; Score 2943; DB 19; Length 579;
Best Local Similarity 99.7%; Pred. No. 3.6e-242;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 MNKLYIGNLSENAAPSDLESIFDKAIPVSGPFLVKTYAFVDCPDSEWALKATEALSGK 60
DB 1 MNKLYIGNLSENAAPSDLESIFDKAIPVSGPFLVKTYAFVDCPDSEWALKATEALSGK 60
QY 61 IELHGKPIEVHSPKQRIRKLIQIRNIPHLQWEVLDSLQVGVVSCQVNTDSETA 120
DB 61 IELHGKPIEVHSPKQRIRKLIQIRNIPHLQWEVLDSLQVGVVSCQVNTDSETA 120
QY 121 VVNTYSSKQARQALDKLNGFQLENFTLVKVAIPDEMAAQNPLQOPRRRGLGQRSS 180
```

```
Db 121 VVNTYSSKQARQALDKLNGFQLENFTLKVAYIDETAQONPLQQPRGRGLGQRSS 180
Qy 181 RQSPGSYSKQPCDPLRLLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
Db 181 RQSPGSYSKQPCDPLRLLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
Qy 241 EKSITILSTPSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300
Db 241 EKSITILSTPSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300
Qy 301 KIEQDTRKITISPLQELTLNPERTITVKGNVETCAKAEEMKKIRESYENDIASMNL 360
Db 301 KIEQDTRKITISPLQELTLNPERTITVKGNVETCAKAEEMKKIRESYENDIASMNL 360
Qy 361 QAHLLPGLNLNALGLFPPTSGMPPTSGPPSAMTPPYQFQESQSETETVHQTFIPALSVGAI 420
Db 361 QAHLLPGLNLNALGLFPPTSGMPPTSGPPSAMTPPYQFQESQSETETVHLFIPALSVGAI 420
Qy 421 IGKQOHIKQLSRFAGASIKIAPAEAPDAKVRMWIITGPPPEAQFKAQGRYIKKEENFV 480
Db 421 IGKQOHIKQLSRFAGASIKIAPAEAPDAKVRMWIITGPPPEAQFKAQGRYIKKEENFV 480
Qy 481 SPKEEVKLEAHRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDQVVVKIT 540
Db 481 SPKEEVKLEAHRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDQVVVKIT 540
Qy 541 GHFYACQVAQRKIQELTQVKHQHQQKALQSGPPQSRRK 579
Db 541 GHFYACQVAQRKIQELTQVKHQHQQKALQSGPPQSRRK 579
```

## RESULT 12

```
US-09-606-421A-348
; Sequence 348, Application US/09606421A
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
```

```
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
```

```
; FILE REFERENCE: 210121.455C9
```

```
; CURRENT APPLICATION NUMBER: US/09/606.421A
```

```
; CURRENT FILING DATE: 2000-06-28
```

```
; NUMBER OF SEQ ID NOS: 354
```

```
; SOFTWARE: FastSEQ for Windows Version 3.0
```

```
; SEQ ID NO 348
```

```
; LENGTH: 579
```

```
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
```

```
US-09-606-421A-348
```

```
Query Match 99.6%; Score 2943; DB 20; Length 579;
```

```
Best Local Similarity 99.7%; Pred. No. 3.6e-242;
```

```
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIALSCK 60
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIALSCK 60
Qy 61 IELHGKPIEVEHSVPKQRIKRLQIRNIPPHLQWEVLDLVLQYGVWESCEQVNTDSETA 120
Db 61 IELHGKPIEVEHSVPKQRIKRLQIRNIPPHLQWEVLDLVLQYGVWESCEQVNTDSETA 120
Qy 121 VVNTYSSKQARQALDKLNGFQLENFTLKVAYIDETAQONPLQQPRGRGLGQRSS 180
```

```
Db 121 VVNTYSSKQARQALDKLNGFQLENFTLKVAYIDETAQONPLQQPRGRGLGQRSS 180
Qy 181 RQSPGSYSKQPCDPLRLLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
Db 181 RQSPGSYSKQPCDPLRLLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
Qy 241 EKSITILSTPSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300
Db 241 EKSITILSTPSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300
Qy 301 KIEQDTRKITISPLQELTLNPERTITVKGNVETCAKAEEMKKIRESYENDIASMNL 360
Db 301 KIEQDTRKITISPLQELTLNPERTITVKGNVETCAKAEEMKKIRESYENDIASMNL 360
Qy 361 QAHLLPGLNLNALGLFPPTSGMPPTSGPPSAMTPPYQFQESQSETETVHQTFIPALSVGAI 420
Db 361 QAHLLPGLNLNALGLFPPTSGMPPTSGPPSAMTPPYQFQESQSETETVHLFIPALSVGAI 420
Qy 421 IGKQOHIKQLSRFAGASIKIAPAEAPDAKVRMWIITGPPPEAQFKAQGRYIKKEENFV 480
Db 421 IGKQOHIKQLSRFAGASIKIAPAEAPDAKVRMWIITGPPPEAQFKAQGRYIKKEENFV 480
Qy 481 SPKEEVKLEAHRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDQVVVKIT 540
Db 481 SPKEEVKLEAHRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDQVVVKIT 540
Qy 541 GHFYACQVAQRKIQELTQVKHQHQQKALQSGPPQSRRK 579
Db 541 GHFYACQVAQRKIQELTQVKHQHQQKALQSGPPQSRRK 579
```

## RESULT 13

```
US-09-630-940A-348
; Sequence 348, Application US/09630940A
; GENERAL INFORMATION:
```

```
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
```

```
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
```

```
; FILE REFERENCE: 210121.455C10
```

```
; CURRENT APPLICATION NUMBER: US/09/630.940A
```

```
; CURRENT FILING DATE: 2000-08-02
```

```
; NUMBER OF SEQ ID NOS: 367
```

```
; SOFTWARE: FastSEQ for Windows Version 3.0
```

```
; SEQ ID NO 348
```

```
; LENGTH: 579
```

```
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
```

```
US-09-630-940A-348
```

```
Query Match 99.6%; Score 2943; DB 20; Length 579;
```

```
Best Local Similarity 99.7%; Pred. No. 3.6e-242;
```

```
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIALSCK 60
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAIALSCK 60
Qy 61 IELHGKPIEVEHSVPKQRIKRLQIRNIPPHLQWEVLDLVLQYGVWESCEQVNTDSETA 120
Db 61 IELHGKPIEVEHSVPKQRIKRLQIRNIPPHLQWEVLDLVLQYGVWESCEQVNTDSETA 120
Qy 121 VVNTYSSKQARQALDKLNGFQLENFTLKVAYIDETAQONPLQQPRGRGLGQRSS 180
```

```
Db 121 VVNTYSSKQARQALDKLNGFQLENFTLVAYIPDEMAAQNPLOQPRGRRLGQRGSS 180
Qy 181 RQSPGVSQKPCDPLRLLLVPTQFVCAIIGKEGATIRNITKOTQSKIDVHRKENAGAA 240
Db 181 RQSPGVSQKPCDPLRLLLVPTQFVCAIIGKEGATIRNITKOTQSKIDVHRKENAGAA 240
Qy 241 EKSTILSTPEGSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300
Db 241 EKSTILSTPEGSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300
Qy 301 KIEODTFTKITSPLQELTYLNPRTITVKGNETCAKAEIEIMKKIRESYENDIASNNL 360
Db 301 KIEODTFTKITSPLQELTYLNPRTITVKGNETCAKAEIEIMKKIRESYENDIASNNL 360
Qy 361 QAHILPGLNMLGLFPPTSGMPPTSGPPSAMTPPYPPQFQSETEVHOFIPALSVCAT 420
Db 361 QAHILPGLNMLGLFPPTSGMPPTSGPPSAMTPPYPPQFQSETEVHOFIPALSVCAT 420
Qy 421 IGKOGHIKQLSRFAGASIKIAPAEADPAKVRMVIITGPPPEAQFKAQGRYKIKENFV 480
Db 421 IGKOGHIKQLSRFAGASIKIAPAEADPAKVRMVIITGPPPEAQFKAQGRYKIKENFV 480
Qy 481 SPKEEVLEAHIRVPSAAGRVIGKGTVNLQNLSSAEVVVPRDQTPDENDQVVKIT 540
Db 481 SPKEEVLEAHIRVPSAAGRVIGKGTVNLQNLSSAEVVVPRDQTPDENDQVVKIT 540
Qy 541 GHFYACQVQAKIOEILTVQKHQOQKALQSGPPQSRK 579
Db 541 GHFYACQVQAKIOEILTVQKHQOQKALQSGPPQSRK 579
```

## RESULT 14

```
US-09-630-940B-348
; Sequence 348, Application US/09630940B
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630,940B
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-630-940B-348
```

```
Query Match 99.6%; Score 2943; DB 20; Length 579;
Best Local Similarity 99.7%; Pred. No. 3.6e-242;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSENAAPSDLESIFDKAKIPVSGPFLVKTYGAFVDCPDSEWALKATEALSGK 60
Db 1 MNKLYIGNLSENAAPSDLESIFDKAKIPVSGPFLVKTYGAFVDCPDSEWALKATEALSGK 60
Qy 61 IELHGKPIEVHSPKQRIRKLIQIRNIPHLQWEVLDSLLVQYGVVESCQVNTDSETA 120
Db 61 IELHGKPIEVHSPKQRIRKLIQIRNIPHLQWEVLDSLLVQYGVVESCQVNTDSETA 120
```

```
Qy 121 VVNTYSSKQARQALDKLNGFQLENFTLVAYIPDEMAAQNPLOQPRGRRLGQRGSS 180
Db 121 VVNTYSSKQARQALDKLNGFQLENFTLVAYIPDEMAAQNPLOQPRGRRLGQRGSS 180
Qy 181 RQSPGVSQKPCDPLRLLLVPTQFVCAIIGKEGATIRNITKOTQSKIDVHRKENAGAA 240
Db 181 RQSPGVSQKPCDPLRLLLVPTQFVCAIIGKEGATIRNITKOTQSKIDVHRKENAGAA 240
Qy 241 EKSTILSTPEGSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300
Db 241 EKSTILSTPEGSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNNFVGRLLIGKEGRNLK 300
Qy 301 KIEODTFTKITSPLQELTYLNPRTITVKGNETCAKAEIEIMKKIRESYENDIASNNL 360
Db 301 KIEODTFTKITSPLQELTYLNPRTITVKGNETCAKAEIEIMKKIRESYENDIASNNL 360
Qy 361 QAHILPGLNMLGLFPPTSGMPPTSGPPSAMTPPYPPQFQSETEVHOFIPALSVCAT 420
Db 361 QAHILPGLNMLGLFPPTSGMPPTSGPPSAMTPPYPPQFQSETEVHOFIPALSVCAT 420
Qy 421 IGKOGHIKQLSRFAGASIKIAPAEADPAKVRMVIITGPPPEAQFKAQGRYKIKENFV 480
Db 421 IGKOGHIKQLSRFAGASIKIAPAEADPAKVRMVIITGPPPEAQFKAQGRYKIKENFV 480
Qy 481 SPKEEVLEAHIRVPSAAGRVIGKGTVNLQNLSSAEVVVPRDQTPDENDQVVKIT 540
Db 481 SPKEEVLEAHIRVPSAAGRVIGKGTVNLQNLSSAEVVVPRDQTPDENDQVVKIT 540
Qy 541 GHFYACQVQAKIOEILTVQKHQOQKALQSGPPQSRK 579
Db 541 GHFYACQVQAKIOEILTVQKHQOQKALQSGPPQSRK 579
```

## RESULT 15

```
US-09-643-597-348
; Sequence 348, Application US/09643597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy R.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-643-597-348
```

```
Query Match 99.6%; Score 2943; DB 20; Length 579;
Best Local Similarity 99.7%; Pred. No. 3.6e-242;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 MNKLYIGNLSENAAPSDLESIFDKAKIPVSGPFLVKTYGAFVDCPDSEWALKATEALSGK 60
Db 1 MNKLYIGNLSENAAPSDLESIFDKAKIPVSGPFLVKTYGAFVDCPDSEWALKATEALSGK 60
Qy 61 IELHGKPIEVHSPKQRIRKLIQIRNIPHLQWEVLDSLLVQYGVVESCQVNTDSETA 120
Db 61 IELHGKPIEVHSPKQRIRKLIQIRNIPHLQWEVLDSLLVQYGVVESCQVNTDSETA 120
```

QY	121	VNVYSSKDQARQALDKLNGFQLENFTLKVAYIPDEMAAQONPLQOPRGRRLGQRGSS	180
Db	121	VNVYSSKDQARQALDKLNGFQLENFTLKVAYIPDEMAAQONPLQOPRGRRLGQRGSS	180
QY	181	ROSGSGSVSKQPCDPLRLLYPTQFVGAIIGKEGATIRNITKOTOSKIDVHRKENAGAA	240
Db	181	ROSGSGSVSKQPCDPLRLLYPTQFVGAIIGKEGATIRNITKOTOSKIDVHRKENAGAA	240
QY	241	EKSITILSTPECTSAACKSILEIMHKEAQDIKFTBEIPLKILAHNNFVGRLLIGKEGRNLK	300
Db	241	EKSITILSTPECTSAACKSILEIMHKEAQDIKFTBEIPLKILAHNNFVGRLLIGKEGRNLK	300
QY	301	KIEQDQDTKITITISPLQELTYLPERTITVKGNVETCAKAEIEIMKKIRESYENDIASMNL	360
Db	301	KIEQDQDTKITITISPLQELTYLPERTITVKGNVETCAKAEIEIMKKIRESYENDIASMNL	360
QY	361	QAHLLPGLNLALGLFPPTSGMPPPTSGPPSAMTPPYQFQSESETVHOFIPALSVGAI	420
Db	361	QAHLLPGLNLALGLFPPTSGMPPPTSGPPSAMTPPYQFQSESETVHOFIPALSVGAI	420
QY	421	IGKQGOHIKQLSRFAGASTIKIAPAEAPDAKVRMVIITGPPEAQKQRIYGIKEENFV	480
Db	421	IGKQGOHIKQLSRFAGASTIKIAPAEAPDAKVRMVIITGPPEAQKQRIYGIKEENFV	480
QY	481	SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDQVVVKIT	540
Db	481	SPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSSAEVVVPRDQTPDENDQVVVKIT	540
QY	541	GHFYACQVNAORKIOEILTQVQKHOQKALQSGPPQSRRK	579
Db	541	GHFYACQVNAORKIOEILTQVQKHOQKALQSGPPQSRRK	579

Search completed: September 29, 2001, 13:59:28  
Job time: 611 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 29, 2001, 13:53:37 ; Search time 358.89 Seconds  
(without alignments)  
71.651 Million cell updates/sec

Title: US-09-466-396A-176  
Perfect score: 2956  
Sequence: 1 MNKLYIGNLSENAAPSDLES.....VKHQKQKALQSGPPQSRRK 579

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 285759 seqs, 44412722 residues

Total number of hits satisfying chosen parameters: 285759

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents\_AA\_New.\*

- 1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2956	100.0	579	US-09-897-778-176	Sequence 176, App
2	2956	100.0	579	US-09-510-376A-176	Sequence 176, App
3	2943	99.6	579	US-09-897-778-348	Sequence 348, App
4	2943	99.6	579	US-09-897-778-446	Sequence 446, App
5	2943	99.6	579	US-09-897-778-449	Sequence 449, App
6	2938	99.4	586	US-09-897-778-427	Sequence 427, App
7	2814	95.2	619	PCT-US01-08631-52322	Sequence 52322, A
8	2733	92.5	583	PCT-US01-08631-42951	Sequence 42951, A
9	2190	74.1	577	US-09-873-637-2	Sequence 2, Appl
10	1950.5	66.0	614	PCT-US01-08631-37153	Sequence 37153, A
11	1946.5	65.8	620	US-09-764-864-1116	Sequence 1116, A
12	1868	63.2	594	PCT-US01-08631-37154	Sequence 37154, A
13	1512	51.2	334	US-09-760-466-1096	Sequence 1096, Ap
14	949	32.1	261	US-09-764-864-1114	Sequence 1114, Ap
15	919	31.1	250	US-09-764-864-1332	Sequence 1332, Ap
16	776.5	26.3	209	PCT-US01-08631-52320	Sequence 52320, A
17	775.5	26.2	266	PCT-US01-08631-42952	Sequence 42952, A
18	626	21.2	171	US-09-764-864-1119	Sequence 1119, Ap
19	551	18.6	148	PCT-US01-08631-52321	Sequence 52321, A
20	543	18.4	132	US-09-760-466-1532	Sequence 1532, Ap
21	527	17.8	192	US-09-764-864-1117	Sequence 1117, Ap
22	474	16.0	93	US-09-864-761-48606	Sequence 48606, A
23	402	13.6	171	US-09-764-864-1536	Sequence 1536, Ap
24	238	8.1	49	US-09-873-637-22	Sequence 22, Appl
25	237	8.0	48	US-09-873-637-24	Sequence 24, Appl
26	232	7.8	49	US-09-873-637-18	Sequence 18, Appl
27	229.5	7.8	627	US-09-760-466-1091	Sequence 1091, Ap

ALIGNMENTS

RESULT 1

US-09-897-778-176

; Sequence 176, Application US/09897778

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Marnerakis, Margarita

; APPLICANT: Fanger, Gary R.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Watanabe, Yoshihiro

; APPLICANT: Henderson, Robert A.

; APPLICANT: Peckham, David W.

; APPLICANT: Fanger, Neil

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C16

; CURRENT APPLICATION NUMBER: US/09/897,778

; CURRENT FILING DATE: 2001-06-28

; NUMBER OF SEQ ID NOS: 467

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 176

; LENGTH: 579

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-897-778-176

Query Match 100.0%; Score 2956; DB 5; Length 579;  
Best Local Similarity 100.0%; Pred. No. 1e-195;  
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MNKL	YIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGTAFVDCPDSEWALKAI	ALSGK	60
Db	1	MNKL	YIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGTAFVDCPDSEWALKAI	ALSGK	60
QY	61	IELH	GKPIEVHSVPRKQRIKQIRNIPHLQWEVLDSLVOYGVVESCQVNTDSE	TA	120
Db	61	IELH	GKPIEVHSVPRKQRIKQIRNIPHLQWEVLDSLVOYGVVESCQVNTDSE	TA	120
QY	121	VNVN	YSSKQDQARQALDKLNGFQLENFTLKVAYIPDEMAAQNPLOQPRGRRGLG	RGSS	180
Db	121	VNVN	YSSKQDQARQALDKLNGFQLENFTLKVAYIPDEMAAQNPLOQPRGRRGLG	RGSS	180
QY	181	RGSG	PSVSKQPCDPLRLLLVPTQFVIGALIGKEGATIRNITKOTSKIDVHR	KENAGAA	240
Db	181	RGSG	PSVSKQPCDPLRLLLVPTQFVIGALIGKEGATIRNITKOTSKIDVHR	KENAGAA	240
QY	241	EKSIT	ILSPGTSACKSILIEIMHKEAQDIKFTTEIPLKILAHNNFVGLICKEGR	NLK	300
Db	241	EKSIT	ILSPGTSACKSILIEIMHKEAQDIKFTTEIPLKILAHNNFVGLICKEGR	NLK	300

```
Qy 301 KIEQDQTKITISPLQELTLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASMNL 360
Db 301 KIEQDQTKITISPLQELTLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASMNL 360
Qy 361 QAHLLPGLNLSNALGLFPPTSGMPPTSGPPSAMTPPYQPFQSESETETVHQFIPALSVCAL 420
Db 361 QAHLLPGLNLSNALGLFPPTSGMPPTSGPPSAMTPPYQPFQSESETETVHQFIPALSVCAL 420
Qy 421 IKGOHILKQLSRFAGASIKIAPAEAPDAKVRMWIITGPPPEAQKAGRIYKGIKEENFV 480
Db 421 IKGOHILKQLSRFAGASIKIAPAEAPDAKVRMWIITGPPPEAQKAGRIYKGIKEENFV 480
Qy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGTVNELQNLSSAEVVPDRDQTPDENQDQVVKIT 540
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGTVNELQNLSSAEVVPDRDQTPDENQDQVVKIT 540
Qy 541 GHFYACQVAQRKIQEILTVKQHQOQKALQSGPPQSRK 579
Db 541 GHFYACQVAQRKIQEILTVKQHQOQKALQSGPPQSRK 579

RESULT 2
US-09-510-376A-176
; Sequence 176, Application US/09510376A
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C7
; CURRENT APPLICATION NUMBER: US/09/510.376A
; CURRENT FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 176
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-510-376A-176
```

```
Query Match 100.0%; Score 2956; DB 5; Length 579;
Best Local Similarity 100.0%; Pred. No. 1e-195;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSNAAPSDLESIFKDAKIPVSGPFLVKTYAFVDCPDDESALKATEALSGK 60
Db 1 MNKLYIGNLSNAAPSDLESIFKDAKIPVSGPFLVKTYAFVDCPDDESALKATEALSGK 60
Qy 61 IELHGKPEVEHSPVKRORIRKLOIRNIPPHLOWEVLDSLLVOYGVVSCQVNTDSETA 120
Db 61 IELHGKPEVEHSPVKRORIRKLOIRNIPPHLOWEVLDSLLVOYGVVSCQVNTDSETA 120
Qy 121 VVNTYSSKQARQALDKLNGFQLENFTLVKVIYIPDEMAAQNPLQOPRGRGLGQSGSS 180
Db 121 VVNTYSSKQARQALDKLNGFQLENFTLVKVIYIPDEMAAQNPLQOPRGRGLGQSGSS 180
Qy 181 RQSPGVSYSKQKPCDLPURLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
Db 181 RQSPGVSYSKQKPCDLPURLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
Qy 241 EKSTILSTPGTSAACKSILEIMHKAQDIFKTEEIPKILAHNNFVGRILIGEGRNLIK 300
Db 241 EKSTILSTPGTSAACKSILEIMHKAQDIFKTEEIPKILAHNNFVGRILIGEGRNLIK 300
Qy 301 KIEQDQTKITISPLQELTLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASMNL 360
Db 301 KIEQDQTKITISPLQELTLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASMNL 360
```

```
Qy 361 QAHLLPGLNLSNALGLFPPTSGMPPTSGPPSAMTPPYQPFQSESETETVHQFIPALSVCAL 420
Db 361 QAHLLPGLNLSNALGLFPPTSGMPPTSGPPSAMTPPYQPFQSESETETVHQFIPALSVCAL 420
Qy 421 IKGOHILKQLSRFAGASIKIAPAEAPDAKVRMWIITGPPPEAQKAGRIYKGIKEENFV 480
Db 421 IKGOHILKQLSRFAGASIKIAPAEAPDAKVRMWIITGPPPEAQKAGRIYKGIKEENFV 480
Qy 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGTVNELQNLSSAEVVPDRDQTPDENQDQVVKIT 540
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGKGGTVNELQNLSSAEVVPDRDQTPDENQDQVVKIT 540
Qy 541 GHFYACQVAQRKIQEILTVKQHQOQKALQSGPPQSRK 579
Db 541 GHFYACQVAQRKIQEILTVKQHQOQKALQSGPPQSRK 579

RESULT 3
US-09-897-778-348
; Sequence 348, Application US/09897778
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897.778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 348
; LENGTH: 579
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-348
```

```
Query Match 99.6%; Score 2943; DB 5; Length 579;
Best Local Similarity 99.7%; Pred. No. 8.1e-195;
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MNKLYIGNLSNAAPSDLESIFKDAKIPVSGPFLVKTYAFVDCPDDESALKATEALSGK 60
Db 1 MNKLYIGNLSNAAPSDLESIFKDAKIPVSGPFLVKTYAFVDCPDDESALKATEALSGK 60
Qy 61 IELHGKPEVEHSPVKRORIRKLOIRNIPPHLOWEVLDSLLVOYGVVSCQVNTDSETA 120
Db 61 IELHGKPEVEHSPVKRORIRKLOIRNIPPHLOWEVLDSLLVOYGVVSCQVNTDSETA 120
Qy 121 VVNTYSSKQARQALDKLNGFQLENFTLVKVIYIPDEMAAQNPLQOPRGRGLGQSGSS 180
Db 121 VVNTYSSKQARQALDKLNGFQLENFTLVKVIYIPDEMAAQNPLQOPRGRGLGQSGSS 180
Qy 181 RQSPGVSYSKQKPCDLPURLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
Db 181 RQSPGVSYSKQKPCDLPURLLVPTQFVGAIIGKEGATIRNITKQTSKIDVHRKENAGAA 240
Qy 241 EKSTILSTPGTSAACKSILEIMHKAQDIFKTEEIPKILAHNNFVGRILIGEGRNLIK 300
Db 241 EKSTILSTPGTSAACKSILEIMHKAQDIFKTEEIPKILAHNNFVGRILIGEGRNLIK 300
Qy 301 KIEQDQTKITISPLQELTLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASMNL 360
Db 301 KIEQDQTKITISPLQELTLNPERTITVKGNETCAKAEIEIMKKIRESYENDIASMNL 360
Qy 361 QAHLLPGLNLSNALGLFPPTSGMPPTSGPPSAMTPPYQPFQSESETETVHQFIPALSVCAL 420
```



Db 361 QAHLIPGLNGLPPTSGMPPPTSGPPSAMTPPYPOFEQSETETVHLFIPALSVGAI 420  
QY 421 IKQGOHILKOLSRFAGASIKIAPAEAPDAKVRMVIITGPPEAQFKAQGRYIGKIEENFV 480  
Db 421 IKQGOHILKOLSRFAGASIKIAPAEAPDAKVRMVIITGPPEAQFKAQGRYIGKIEENFV 480  
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGGKTVNELONLSSAEVVVPRDQTPDENDQVVVKIT 540  
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGGKTVNELONLSSAEVVVPRDQTPDENDQVVVKIT 540  
QY 541 GHFYACQVAORQIQLTQVKOHQOKALQSGPPQSRRK 579  
Db 541 GHFYACQVAORQIQLTQVKOHQOKALQSGPPQSRRK 579

RESULT 4  
US-09-897-778-446  
; Sequence 446, Application US/09897778  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Marnerakis, Margarita  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Peckham, David W.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C16  
; CURRENT APPLICATION NUMBER: US/09/897,778  
; CURRENT FILING DATE: 2001-06-28  
; NUMBER OF SEQ ID NOS: 467  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 446  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-897-778-446

Query Match 99.6%; Score 2943; DB 5; Length 579;  
Best Local Similarity 99.7%; Pred. No. 8.1e-195;  
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAEALSCK 60  
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAEALSCK 60  
QY 61 IELHGKPIEVHSVPRQRIRKLIQIRNIPHLQWEVLDSLLVQYGVVSECEQVNTDSETA 120  
Db 61 IELHGKPIEVHSVPRQRIRKLIQIRNIPHLQWEVLDSLLVQYGVVSECEQVNTDSETA 120  
QY 121 VNVVTSSKDOARQALDKLNGFQLENFTLKVAYIPDEMAAQNPLOQPRRGLGQSGSS 180  
Db 121 VNVVTSSKDOARQALDKLNGFQLENFTLKVAYIPDEMAAQNPLOQPRRGLGQSGSS 180  
QY 181 ROGSPGSVKQKPCDPLRLVPTQFVGALIGKEGATIRNITKQTSKIDVHRKENAGAA 240  
Db 181 ROGSPGSVKQKPCDPLRLVPTQFVGALIGKEGATIRNITKQTSKIDVHRKENAGAA 240  
QY 241 EKSITILSTPEGSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNFVGRGLIGKEGRNLK 300  
Db 241 EKSITILSTPEGSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNFVGRGLIGKEGRNLK 300  
QY 301 KIEQDQDTKITISPLQELTYLNPERTITVKGNVETCAKAEETIMKKIRESYENDIASMNL 360  
Db 301 KIEQDQDTKITISPLQELTYLNPERTITVKGNVETCAKAEETIMKKIRESYENDIASMNL 360  
QY 361 QAHLIPGLNGLPPTSGMPPPTSGPPSAMTPPYPOFEQSETETVHLFIPALSVGAI 420

Db 361 QAHLIPGLNGLPPTSGMPPPTSGPPSAMTPPYPOFEQSETETVHLFIPALSVGAI 420  
QY 421 IKQGOHILKOLSRFAGASIKIAPAEAPDAKVRMVIITGPPEAQFKAQGRYIGKIEENFV 480  
Db 421 IKQGOHILKOLSRFAGASIKIAPAEAPDAKVRMVIITGPPEAQFKAQGRYIGKIEENFV 480  
QY 481 SPKEEVKLEAHIRVPSFAAGRVIGGKTVNELONLSSAEVVVPRDQTPDENDQVVVKIT 540  
Db 481 SPKEEVKLEAHIRVPSFAAGRVIGGKTVNELONLSSAEVVVPRDQTPDENDQVVVKIT 540  
QY 541 GHFYACQVAORQIQLTQVKOHQOKALQSGPPQSRRK 579  
Db 541 GHFYACQVAORQIQLTQVKOHQOKALQSGPPQSRRK 579

RESULT 5  
US-09-897-778-449  
; Sequence 449, Application US/09897778  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Marnerakis, Margarita  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Carter, Darrick  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Peckham, David W.  
; APPLICANT: Fanger, Neil  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C16  
; CURRENT APPLICATION NUMBER: US/09/897,778  
; CURRENT FILING DATE: 2001-06-28  
; NUMBER OF SEQ ID NOS: 467  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 449  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-897-778-449

Query Match 99.6%; Score 2943; DB 5; Length 579;  
Best Local Similarity 99.7%; Pred. No. 8.1e-195;  
Matches 577; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAEALSCK 60  
Db 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKTGYAFVDCPDSEWALKAEALSCK 60  
QY 61 IELHGKPIEVHSVPRQRIRKLIQIRNIPHLQWEVLDSLLVQYGVVSECEQVNTDSETA 120  
Db 61 IELHGKPIEVHSVPRQRIRKLIQIRNIPHLQWEVLDSLLVQYGVVSECEQVNTDSETA 120  
QY 121 VNVVTSSKDOARQALDKLNGFQLENFTLKVAYIPDEMAAQNPLOQPRRGLGQSGSS 180  
Db 121 VNVVTSSKDOARQALDKLNGFQLENFTLKVAYIPDEMAAQNPLOQPRRGLGQSGSS 180  
QY 181 ROGSPGSVKQKPCDPLRLVPTQFVGALIGKEGATIRNITKQTSKIDVHRKENAGAA 240  
Db 181 ROGSPGSVKQKPCDPLRLVPTQFVGALIGKEGATIRNITKQTSKIDVHRKENAGAA 240  
QY 241 EKSITILSTPEGSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNFVGRGLIGKEGRNLK 300  
Db 241 EKSITILSTPEGSTSAACKSILEIMHKEAQDIKFTTEIPLKILAHNFVGRGLIGKEGRNLK 300  
QY 301 KIEQDQDTKITISPLQELTYLNPERTITVKGNVETCAKAEETIMKKIRESYENDIASMNL 360  
Db 301 KIEQDQDTKITISPLQELTYLNPERTITVKGNVETCAKAEETIMKKIRESYENDIASMNL 360  
QY 361 QAHLIPGLNGLPPTSGMPPPTSGPPSAMTPPYPOFEQSETETVHLFIPALSVGAI 420  
Db 361 QAHLIPGLNGLPPTSGMPPPTSGPPSAMTPPYPOFEQSETETVHLFIPALSVGAI 420

QY	421	IGQGOHHIQLSRFAGASTIKIAPAEAPDAKVRVVIITGPPPEAQFKAQGRHYKIKIEENFV	480
Db	421	IGQGOHHIQLSRFAGASTIKIAPAEAPDAKVRVVIITGPPPEAQFKAQGRHYKIKIEENFV	480
QY	481	SPKEEVKLEAHIRVPSFAAGRVIGKGCKTVNELQNLSSAEVVVPRDQTPDENQVVKIT	540
Db	481	SPKEEVKLEAHIRVPSFAAGRVIGKGCKTVNELQNLSSAEVVVPRDQTPDENQVVKIT	540
QY	541	GHFYACVQAQRKTQEILTVKHQQHQAALQSGPPQSRKK	579
Db	541	GHFYACVQAQRKTQEILTVKHQQHQAALQSGPPQSRKK	579

```

RESULT      6
US-09-897-778-427
; Sequence 427, Application US/09897778
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C16
; CURRENT APPLICATION NUMBER: US/09/897,778
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 427
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-897-778-427

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[illegible]

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QY      422 GKGOQHIKQLSRFAGASIKIAPAEADPAKVRWVIITGPPPEAQFKAQGRIYKGKIENFVS 481
Db      429 GKGOQHIKQLSRFAGASIKIAPAEADPAKVRWVIITGPPPEAQFKAQGRIYKGKIENFVS 488
QY      482 PKEEVKLEAHIRVSPFAAGRVICGGKTVNELQNLSAEVVVPDQTDPENDOVVKITG 541
Db      489 PKEEVKLEAHIRVSPFAAGRVICGGKTVNELQNLSAEVVVPDQTDPENDOVVKITG 548
QY      542 HFYACQVAQRKIQEILTQVKHQHQQOKALQSGPPQSRRK 579
Db      549 HFYACQVAQRKIQEILTQVKHQHQQOKALQSGPPQSRRK 586

RESULT 7
PCT-US01-08631-52322
; Sequence 52322, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 52322
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (542)..(554)
; OTHER INFORMATION: KH domain proteins family of RNA binding proteins domain
; OTHER INFORMATION: Identified by eMATRIX, accession number PF00013, p-value=1.000
; OTHER INFORMATION: raw score of 5.78
; NAME/KEY: DOMAIN
; LOCATION: (244)..(587)
; OTHER INFORMATION: KH domain identified by Pfam, accession name KH-domain, E-
; OTHER INFORMATION: value=1.5e-41, Pfam score of 151.5
; NAME/KEY: misc_feature
; LOCATION: (1)...(619)
; OTHER INFORMATION: xaa = X or * as defined in Table 2
PCT-US01-08631-52322
```

Query Match	95.2%;	Score 2814;	DB 1;	Length 619;
Best Local Similarity	95.0%;	Pred. No. 6.8e-186;		
Matches 554; Conservative	8;	Mismatches 17;	Indels 4;	Gaps
<hr/>				
QY	1	MNKLIGNLSENAAPSDLESIEFKDAKIPVSGPFLVKTYGFVDCPDSEWALKAIAESLK 60		
Db	37	MNKLIGNLSENAAPSDLKSIEFKDAKIPVSGPFLVKTYGFVDCPDSEWALRAIKAFSGK 96		
QY	61	IELHGKPIEVEHSVPKRQRIRLQLRINTPPHLOWEVLDLSLLVOYGVSCEQVNTDSETA 120		
Db	97	IELHGKPIEVEHSVPKRQRIRLQLRINTPPHLOWEVLDLSLLVOYGVSCEQVNTDSETA 156		
QY	121	VNVVTYSKKDQARQA-----LDKLNGFQLNFETLKVAYTPDENAAQNPLQQPRGRGLQG 176		
Db	157	VNVVTYSKKDQARQALDKLLDKLNGFQLNFETLKVAYTPDENATQONFLQPRGRGLQG 216		
QY	177	RGSSRGSPGSVSKQPCDLPRLVLPTQFVGAIIGKEGATIRNTTKQTOKIDVHRKEN 236		
Db	217	RGSSRGSPGSVSKQPCDSPRLVLPTQFVGAIIGKEGATIRNTTKQTOKIDVHRKEN 276		
QY	237	AGAAEKSIITLPSTPGTSAACKSILEIMHKEAQDIKFTEEIPCLKTLAHNNFVGRILIGREG 296		
Db	277	AGAAEKSIITLPSTPGTSAACKSILEIMHKEAQDIKFTEEIPCLKTLAHNNFVGRILIGREG 336		
QY	297	RNLKKIEQDTDKIITSPLQEULTYNPERTIVFGNVETCAKAEIEIWKIKRESYENDIA 356		

Db 337 RNLKKIEQDQTKITISPLQELTLNPNERTITVKGNETCAKAEIEIMKKIRRESYENDIA 396  
QY 357 SNLQAHILIPGLNALGLFPPTSGMPPTSGPPSAMTPPPYQFQSESETVHQFIPALS 416  
Db 397 SNLQAHILIPGLNALGLFPPTSGMPPTSGPPSAMTPPPYQFQSESETVHQFIPALS 456  
QY 417 VCAITGKOGHITKQLSRFAGASIKITAPAEADAKVVMVLIITGPPAQAQRIYGIKE 476  
Db 457 VRALISKOGHITKQLSRFAGASSKIAPVEADPAKVRVMVLIAGSPARFKAQRIYGIKE 516  
QY 477 ENFVSPKEEVKLEAHIRVPSFAAGRVIGKGTVMNELQNLSSAEVVPDQTPDENDQVV 536  
Db 517 ENFVSPKEEVKLEAHIRVPSFAAGRVIGKGTVMNELQNLSSAEVVPDQTPDENDQVV 576  
QY 537 VKITGHFYACQVAQKRIQIBELITQVQHQQKALQSGPPQSRKK 579  
Db 577 VKITGHFYACQVAQKRIQIBELITQVQHQQKALQSGPPQSRKK 619

## RESULT 8

PCT-US01-08631-42951  
; Sequence 42951, Application PC/TUS0108631  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-049  
; CURRENT APPLICATION NUMBER: PCT/US01/08631  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 42951  
; LENGTH: 583  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (504)...(516)  
; OTHER INFORMATION: KH domain proteins family of RNA binding proteins domain  
; OTHER INFORMATION: Identified by eMATRIX, accession number PF00013, p-value=1.000e-1  
; OTHER INFORMATION: raw score of 5.78  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(583)  
; OTHER INFORMATION: Xaa = X or \* as defined in Table 2  
PCT-US01-08631-42951

Query Match 92.5%; Score 2733; DB 1; Length 583;  
Best Local Similarity 92.8%; Pred. No. 2.4e-180;  
Matches 541; Conservative 6; Mismatches 33; Indels 4; Gaps 1;

QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKYGVAFVDCPDSEWALKAIKALSCK 60  
Db 1 MNKPYIRNLSENAAPDLDELIGILKDAKIPVSGPFLVKYGVAFVDCPDSEWALKAIKALSCK 60  
QY 61 IELHGKPIEVHSVPKRORIRKLRQIRNIPPHLOWEVLDSLLVQYGVVSECEQVNTDSETA 120  
Db 61 IELHGKPIEVHSVPKRORIRKLRQIRNIPPHLOWEVLDSLLVQYGVVSECEQVNTDSETA 120  
QY 121 VVNVTYSSKQDQARQALDKLNGFQLENFTLKVAYIPDEMAAQNPLQOPRGRGLQ 176  
Db 121 VVNVTYSSKQDQARQALDKLNGFQLENFTLKVAYIPDEMAAQNPLQOPRGRGLQ 180  
QY 177 RGSRGSGPSVSKQKPCDLPLRLVPTQFVGAIIGKEGATIRNITKTQSKIDVHRKEN 236  
Db 181 RGSRGSGPSVSKQKPCDLPLRLVPTQFVGAIIGKEGATIRNITKTQSKIDVHRKEN 240  
QY 237 AGAAEKSTILSTPGTSAACKSILEIMHKEAQDITKFTTEIPLKILAHNNFVGRLLIGKEG 296  
|||||

Db 241 AGAAEKSTILSTPGTSAACKSILEIMHKEAQDITKFTTEIPLKILAHNNFVGRLLIGKEG 300  
QY 297 RNLKKIEQDQTKITISPLQELTLNPNERTITVKGNETCAKAEIEIMKKIRRESYENDIA 356  
Db 301 RNLKKIEQDQTKITISPLQELTLNPNERTITVKGNETCAKAEIEIMKKIRRESYENDIT 360  
QY 357 SNLQAHILIPGLNALGLFPPTSGMPPTSGPPSAMTPPPYQFQSESETVHQFIPALS 416  
Db 361 SNLQAHILIPGLNALGLFPPTSGMPPTSGPPSAMTPPPYQFQSESETVHQFIPALS 420  
QY 417 VCAITGKOGHITKQLSRFAGASIKITAPAEADAKVVMVLIITGPPAQAQRIYGIKE 476  
Db 421 VRALISKOGHITKQLSRFAGASSKIAPVEADPAKVRVMVLIAGSPARFKAQRIYGIKE 480  
QY 477 ENFVSPKEEVKLEAHIRVPSFAAGRVIGKGTVMNELQNLSSAEVVPDQTPDENDQVV 536  
Db 481 ENFVSPKEEVKLEAHIRVPSFAAGRVIGKGTVMNELQNLSSAEVVPDQTPDENDQVV 540  
QY 537 VKITGHFYACQVAQKRIQIBELITQVQHQQKALQSGPPQSRKK 579  
Db 541 VKITGHFYACQVAQKRIQIBELITQVQHQQKALQSGPPQSRKK 583

## RESULT 9

US-09-873-637-2  
; Sequence 2, Application US/09873637  
; GENERAL INFORMATION:  
; APPLICANT: Ross, Jeffrey  
; TITLE OF INVENTION: THE C-MYC CODING REGION DETERMINANT-BINDING PROTEIN  
; TITLE OF INVENTION: (CRD-BP) AND ITS NUCLEIC ACID SEQUENCE  
; FILE REFERENCE: 960296.95131  
; CURRENT APPLICATION NUMBER: US/09/873,637  
; CURRENT FILING DATE: 2001-06-04  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 577  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-873-637-2

Query Match 74.1%; Score 2190; DB 5; Length 577;  
Best Local Similarity 74.1%; Pred. No. 5.7e-143;  
Matches 434; Conservative 62; Mismatches 74; Indels 16; Gaps 8;

QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPFLVKYGVAFVDCPDSEWALKAIKALSCK 60  
Db 1 MNKLYIGNLSENVTPADLEKVFAEHKSISYSGQFLVKSGYAFVDCPDSEWALKAIKALSCK 60  
QY 61 IELHGKPIEVHSVPKRORIRKLRQIRNIPPHLOWEVLDSLLVQYGVVSECEQVNTDSETA 120  
Db 61 VELOKRLMEHSEHVPKQSRKRIQIRNIPPLRWEVLDSLLAQYGVNCEQVNTSEETA 120  
QY 121 VVNVTYSSKQDQARQALDKLNGFQLENFTLKVAYIPDEMAAQNPLQOPRGRGLQ 179  
Db 121 VVNVTYSSKQDQARQALDKLNGFQLENFTLKVAYIPDEMAAQNPLQOPRGRGLQ 176  
QY 180 SRQSGP---GSVSKQKPCDLPLRLVPTQFVGAIIGKEGATIRNITKTQSKIDVHRKEN 236  
Db 177 PRQGSFVAAGAPAKQOPVDIPLRLVPTQFVGAIIGKEGATIRNITKTQSKIDVHRKEN 236  
QY 237 AGAAEKSTILSTPGTSAACKSILEIMHKEAQDITKFTTEIPLKILAHNNFVGRLLIGKEG 296  
Db 237 AGAAEKSTILSTPGTSAACKSILEIMHKEAQDITKFTTEIPLKILAHNNFVGRLLIGKEG 296  
QY 297 RNLKKIEQDQTKITISPLQELTLNPNERTITVKGNETCAKAEIEIMKKIRRESYENDIA 356  
Db 297 RNLKKIEQDQTKITISPLQELTLNPNERTITVKGNETCAKAEIEIMKKIRRESYENDIA 356  
QY 357 SNLQAHILIPGLNALGLFPPTSGMPPTSGPPSAMTPPPYQFQSESETVHQFIP 413  
Db 357 AMSLSHLIPGLNLAAGLVGFPAASSAVPP---PPSVTGAAPYSSFMQAEQEVQVFI 413



QY 397 YPOFEQ-SETETVHQIPALSGALIGKQOHKQLSRFAGASIKIAPAEAPDAKVRMVI 455  
Db 439 FPHHSYPOEIVNLFIPTQAVGAIIGKGAHIKQLARFAGASIKIAPAEAPDAKVRMVI 498  
QY 456 ITGPPPEAKQAQRIYKGIKEENFVSPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQN 515  
Db 499 ITGPPPEAKQAQRIYKGIKEENFVSPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQN 558  
QY 516 LSSAEVVVPRDQTPDENQVVKITGHFYACQVAQRKIQEILITQVKOHQOO 566  
Db 559 LTSAEIVPRDQTPDENEEVIRIIGHFFASQTAQRKIREIVQVQKQEQK 609

RESULT 12  
PCT-US01-08631-37154  
; Sequence 37154, Application PC/TUS0108631  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-049  
; CURRENT APPLICATION NUMBER: PCT/US01/08631  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/549,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 37154  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: DOMAIN  
; LOCATION: (43)..(62)  
; OTHER INFORMATION: Eukaryotic RNA-binding region RNP-1 proteins domain  
; OTHER INFORMATION: identified by eMATRIX, accession number BL00030A, p-value=4.938e-  
; OTHER INFORMATION: 12, raw score of 14.39  
; NAME/KEY: DOMAIN  
; LOCATION: (235)..(558)  
; OTHER INFORMATION: KH domain identified by Pfam, accession name KH-domain, E-  
; OTHER INFORMATION: value=1.8e-51, Pfam score of 184.4  
PCT-US01-08631-37154

Query Match 63.2%; Score 1868; DB 1; Length 594;  
Best Local Similarity 64.8%; Pred. No. 8.8e-121;  
Matches 368; Conservative 78; Mismatches 96; Indels 26; Gaps 6;

QY 1 MNKLYIGNLSENAAPSDLESIFKDAKIPVSGPPLVKTGVAFYDCPDSEWALKAEALSGK 60  
Db 40 MNKLYIGNLSPAVTADLRQLFGDRKLPLAGQVLLKSGYAFVDPQNWAIKRAIETLSGK 99  
QY 61 IELHGKPIEVHEVSPKRRKQIRNIPHLQWELDSLIVQYGVVSECEQVNTDETA 120  
Db 100 VELHGKIMEVDYISVSKRLKQIRNIPHLQWELDGLLAQYGVNVEQVNTDETA 159  
QY 121 VNVVTYSSKDOARQALDKLNGFLENFTLKVAYIPDEMAAQNPLOQPRGRRLGORGSS 180  
Db 160 VNVVTATREEAKIAMEKLSGHQFENYSEKISVIPDEEVSSPPQ--RAQR--GDHSSR 215  
QY 181 RQG-SPGVSVKQPCDLPURLLVPTQFVGAIGKEGATRNITKQTSKIDVHRKENAGA 239  
Db 216 EQGHAPGTSQARQIDFPLRLVPTQFVGAIGKEGATRNITKQTSKIDVHRKENAGA 275  
QY 240 AKSITILTSPECTSACKSILEIMHKEADIKFTTEIPLKILAHNNFVCRLLGKEGRNL 299  
Db 276 AEPVTHATPECTSEACRMILSIKQEADETKLAEIPLKILAHNGLVCRLLGKEGRNL 335  
QY 300 KKIEQDQTDKITISPLQELTYNPRTITVKGNETCAKAEIEMKKIRSYENDIASMN 359  
Db 336 KKIEHETGKITISSLQDLISYNPRTITVKGNETCAKAEIEMKKILREAFENDMLAVN 395

QY 360 LQAHILPGLNLNALGLFPPTSGMPPTSGPPSAMTPPYPOFEQ-SETETVHQIPALSVG 418  
Db 396 THS-----GTF-----SSLYPHHQFGFPFHHHSYPOEIVNLFIPTQAVG 435  
QY 419 AIIIGKQOHKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAKQAQRIYKGIKEEN 478  
Db 436 AIIIGKGAHIKQLARFAGASIKIAPAEAPDAKVRMVIITGPPPEAKQAQRIYKGIKEEN 495  
QY 479 FVSPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSAEVVVPRDQTPDENQVVK 538  
Db 496 FPNPKEEVKLEAHIRVPSSTAGRVIGKGGKTVNELQNTSAEIVPRDQTPDENEEVIVR 555  
QY 539 ITGHFYACQVAQRKIQEILITQVKOHQOO 566  
Db 556 IIGHFFASQTAQRKIREIVQVQKQEQK 583

RESULT 13  
US-09-760-466-1096  
; Sequence 1096, Application US/09760466  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: P7259  
; CURRENT APPLICATION NUMBER: US/09/760,466  
; CURRENT FILING DATE: 2001-01-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1813  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1096  
; LENGTH: 334  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (318)  
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (330)  
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids  
US-09-760-466-1096

Query Match 51.2%; Score 1512; DB 5; Length 334;  
Best Local Similarity 96.5%; Pred. No. 1.2e-96;  
Matches 300; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 228 KIDVHRKENAGAAEKSTITILSTPEGTSAAKSSILEIMHKEAQDIKFTTEIPLKILAHNF 287  
Db 24 RIDVHRKENAGAAEKSTITILSTPEGTSAAKSSILEIMHKEAQDIKFTTEIPLKILAHNF 83  
QY 288 VGRLLCKEGRNLKKIEQDQTDKITISPLQELTYNPRTITVKGNETCAKAEIEMKKI 347  
Db 84 VGRLLCKEGRNLKKIEQDQTDKITISPLQELTYNPRTITVKGNETCAKAEIEMKKI 143  
QY 348 RESYENDIASMNLOAHILPGLNLNALGLFPPTSGMPPTSGPPSAMTPPYPOFEQSETET 407  
Db 144 RESYENDIASMNLOAHILPGLNLNALGLFPPTSGMPPTSGPPSAMTPPYPOFEQSETET 203  
QY 408 VHOIFALSVGAIIGKQOHKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAKQAQ 467  
Db 204 VHLFIPLSVGAIIGKQOHKQLSRFAGASIKIAPAEAPDAKVRMVIITGPPPEAKQAQ 263  
QY 468 GRIYGIKEENFVSPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSAEVVVPRDQ 527  
Db 264 GRIYGIKEENFVSPKEEVKLEAHIRVPSFAAGRVIGKGGKTVNELQNLSAEVVVPRDQ 323  
QY 528 TPDENQVVK 538  
Db 324 HLMRMDXVVK 334

RESULT 14

US-09-764-864-1114

; Sequence 1114, Application US/09764864  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT223  
; CURRENT APPLICATION NUMBER: US/09/764,864  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1792  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1114  
; LENGTH: 261  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-764-864-1114

Query Match 32.1%; Score 949; DB 5; Length 261;  
Best Local Similarity 74.5%; Pred. No. 4.9e-58;  
Matches 193; Conservative 26; Mismatches 32; Indels 8; Gaps 5;

QY 324 ERTITVKNVETCAKAEIEIMKKIRESYENDIASNMQAHLIPGLNLNALGLFPPTSGMP 383  
DB 8 ERTITVKAINECCRAEQEIMKKVREAYENDVAAMSLQSHLIPGLNLAAVGLFPASSAV 67  
QY 384 PPTSGPPSMT--PPYPOFEQS-ETETVHOFTIPALSVGAIIKQGOHIKQLSRFAGASIK 440  
DB 68 PP---PPSSVTGAAPYSSFMQAPQEQEMVQVFIQAQAVGAIIGKKGHIKQLSRFASASIK 124  
QY 441 IAPAEAPDAKVRMWIITGPPPEAQKAGRIYCKIKEENFVSPKEEVKLEAHIRVPSFAAG 500  
DB 125 IAPETPSKVRMWIITGPPPEAQKAGRIYCKIKEENFVSPKEEVKLEAHIRVPSAAG 184  
QY 501 RVIGKGTVNLQNLSSAEVVPDQTPDENDQVVKITGHFYACQVAQRKIQIILTQV 560  
DB 185 RVIGKGTVNLQNLTAEEVVPDQTPDENDQVVKITGHFYASQMAQRKIRDLAQV 244  
QY 561 KOHQKALQSGPPQSRRK 579  
DB 245 KQ-QHQKG-QSNOQAARRK 261

## RESULT 15

US-09-764-864-1532  
; Sequence 1532, Application US/09764864  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT223  
; CURRENT APPLICATION NUMBER: US/09/764,864  
; CURRENT FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1792  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1532  
; LENGTH: 250  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (127)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (134)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-764-864-1532

Query Match 31.1%; Score 919; DB 5; Length 250;  
Best Local Similarity 73.3%; Pred. No. 5.3e-56;  
Matches 187; Conservative 26; Mismatches 34; Indels 8; Gaps 5;

QY 328 TVKGNVETCAKAEIEIMKKIRESYENDIASNMQAHLIPGLNLNALGLFPPTSGMPPTS 387  
DB 1 TVKGAINECCRAEQEIMKKVREAYENDVAAMSLQSHLIPGLNLAAVGLFPASSAVPP-- 58  
QY 388 GPPSMT--PPYPOFEQS-ETETVHOFTIPALSVGAIIKQGOHIKQLSRFAGASIKIAPA 444  
DB 59 -PPSSVTGAAPYSSFMQAPQEQEMVQVFIQAQAVGAIIGKKGHIKQLSRFASASIKIAPP 117  
QY 445 EAPDAKVRMWIITGPPPEAQKAGRIYCKIKEENFVSPKEEVKLEAHIRVPSFAAGRVIG 504  
DB 118 ETPDSKVRMWIITGPPPEAQKAGRIYCKIKEENFVSPKEEVKLEAHIRVPSAAGRVIG 177  
QY 505 KGGKTVNLQNLSSAEVVPDQTPDENDQVVKITGHFYACQVAQRKIQIILTQVQKHQ 564  
DB 178 KGGKTVNLQNLTAEEVVPDQTPDENDQVVKITGHFYASQMAQRKIRDLAQVKQ-Q 236  
QY 565 QKALQSGPPQSRRK 579  
DB 237 HQKG-QSNOQAARRK 250

Search completed: September 29, 2001, 14:05:40  
Job time: 723 sec







OM of: US-09-466-396A-176 to: Pending\_Patents\_NA\_Main:\* out\_format : pfs

Date: Sep 29, 2001 3:40 PM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

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Command line parameters:
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-DB=Patenting_Patents_NA_Main -QFMT=fastap -SUFFIX=rxnm
-GAPOP=12,000 -GAPEXT=4,000 -MINMATCH=0.100 -LOOPCEL=0.000
-LOOPEXT=0.000 -QGAPOP=4,500 -QGAPEXT=0.050 -XGAPOP=10.000
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-MATRIX=blosom62 -TRANS=human40_cdi -LIST=45 -DOCALLIGN=200
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-OUTFMT=pis -NORM=ext -MINLEN=0 -MAXLEN=2000000000
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; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng
; APPLICANT: Gure, Ali
; APPLICANT: Tsang, Solam
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Jager, Elke
; APPLICANT: Knuth, Alexander
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
; TITLE OF INVENTION: Antigen, The Antigens Per Se, And Uses Thereof
; FILE REFERENCE: LUD 5338
; CURRENT APPLICATION NUMBER: US/09/061,709B
; CURRENT FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 4
; LENGTH: 4159
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; US-09-061-709-4

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67 orLeGluValGluHisSerValProLysArgGlnArgIleArgLysLeuG 84
451 CATAGAAGTTGAGCACTCGGTCGCCAAAAGCAAGGATTTCGGAACATTC 500

84 InIleArgAsnIleProProHisLeuGlnTrpGluValLeuAspSerLeu 100
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501 AGATACGAATAATCCCGCCCTCATTTTACGTGGGAGGTGCTGGATAGTTTA 550

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117 rGluThrAlaValValAsnValThrTyrSerSerLysAspGlnAlaArgG 134
601 GGAACCTGCAGTTGTAATGTAACTGTAACCTATTTCAGTTAAGNCAAGCTAGAC 650

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167 nProArgGlyArgGlyLeuGlyGlnArgGlySerArgGlnGlyS 184
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301 LysIleGluGlnAspThrAspThrLysIleThrIleSerProLeuGlnG1 317
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384 roProThrSerGlyProProSerAlaMetThrProProTyrProGlnPhe 400
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417 lclyAlaIleLeuGlyLysGlnGlnHisIleLysGlnLeuSerArgp 434
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551 ArgLysIleGlnGluIleLeuThrGlnValLysGlnHisGlnGlnGlnly 567
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: GENERAL INFORMATION:  
: APPLICANT: Chen, Yao-Tseng  
: APPLICANT: Gure, Ali  
: APPLICANT: Tsang, Solam  
: APPLICANT: Stockert, Elisabeth  
: APPLICANT: Jager, Elke  
: APPLICANT: Knuth, Alexander  
: APPLICANT: Old, Lloyd J.  
: TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated Ant  
: TITLE OF INVENTION: Antigens Per Se, And Uses Thereof  
: FILE REFERENCE: LUD 5538.1 PCT  
: CURRENT APPLICATION NUMBER: US/09/270,437A  
: CURRENT FILING DATE: 1999-03-16  
: NUMBER OF SEQ ID NOS: 8  
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: TYPE: DNA  
: ORGANISM: Homo sapiens  
: FEATURE:  
US-09-270-437-4

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34 euValLysThrGlyTyrAlaPheValAspCysProAspGluSerTrpAla 50
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351 TGGTGAAGACTGGCTACGGCTTCGGTGGAGTGGCCCGGACGAGAGCTGG 400
51 LeuLysAlaIleGluAlaLeuSerGlyLysIleGluLeuHisGlyLysPr 67
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351 TyrGluAsnAspIleAlaSerMetAsnLeuGlnAlaHisLeuIleProG 367
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1301 TATGAANAATGATATTGCTTCTATGAATCTTCAAGCACATTTAATTCCT 1350
367 yLeuAsnLeuAsnAlaLeuGlyLeuPheProProThrSerGlyMetProp 384
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451 ValArgMetValIleIleThrGlyProProGluAlaGlnPheLysAlaGl 467
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551 ArgLysIleGlnGluIleLeuThrGlnValLysGlnHisGlnGlnGlnLy 567
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1901 AGAAAAATTCAGGAATTCAGCTCAGTAAAGCAGCACCACCAACAGAA 1950
567 sAlaLeuGlnSerGlyProProGlnSerArgArgLys 579
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; Sequence 175, Application US/09466396A  
; GENERAL INFORMATION:  
; APPLICANT: Wang, TongLong  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND

;; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
;; FILE REFERENCE: 210121.455C4  
;; CURRENT APPLICATION NUMBER: US/09/466,396A  
;; CURRENT FILING DATE: 1999-12-17  
;; NUMBER OF SEQ ID NOS: 224  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 175

;; LENGTH: 4181

;; TYPE: DNA

;; ORGANISM: Homo sapiens

;; FEATURE:

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;; LOCATION: (3347)

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;; NAME/KEY: unsure

;; LOCATION: (4115)

;; OTHER INFORMATION: n=A,T,C or G

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Ratio: 5.105 Gaps: 0  
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Align seg 1/1 to: US-09-466-396A-175 from: 1 to: 4181

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17 PleuGluSerIlePheLeuAspAlaLysIleProValSerGlyProPheL 34  
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301 CTAGAAAGTATCTTCAAGGACGCCCAAGATCCCGGTGTCGGGACCTTCC 350  
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601 GGAACTCGAGTGTAAATGTAACTATTCAGTAAGGACCAAGCTAGAC 650  
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; APPLICANT: Wang, TongLong  
; APPLICANT: Fan, Lique

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; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy A.  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY  
; FILE REFERENCE: 210121.455C8  
; CURRENT APPLICATION NUMBER: US/09/542,615A  
; CURRENT FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 350  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 175  
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; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangor, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606.421A
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 354
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; TYPE: DNA
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: GENERAL INFORMATION:  
: APPLICANT: Wang, Tongtong  
: APPLICANT: Fan, Liqun  
: APPLICANT: Kalos, Michael D.  
: APPLICANT: Bangur, Chaitanya S.  
: APPLICANT: Hosken, Nancy  
: APPLICANT: Fanger, Gary R.  
: APPLICANT: Li, Samuel X.  
: APPLICANT: Wang, Aijun  
: APPLICANT: Skeiky, Yasir A.W.  
: APPLICANT: Henderson, Robert A.  
: APPLICANT: McNeill, Patricia D.  
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
: FILE REFERENCE: 210121.455C10  
: CURRENT APPLICATION NUMBER: US/09/630,940A  
: CURRENT FILING DATE: 2000-08-02  
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US-09-630-940A-175

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  Ratio: 5.105          Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

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US-09-466-396A-176 x US-09-630-940A-175
Align seg 1/1 to: US-09-630-940A-175 from: 1 to: 4181

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251 ATGACAACTGTATATCGAAGCTCAGGAGACGCCGCCCTCGGA 300
17 pLeuGluSerIlePheLysAspAlaLysIleProValSerGlyProPheL 34
301 CCTAGAAAGTATCTTCAAGGACGCCAAGATCCCGGTGTCGGGACCCCTCC 350
34 euValLysThrGlyTyrAlaPheValAspCysProAspGluSerTrpAla 50
351 TGGTCAAGACTGGCTACGCGCTTCGTGACTGCCCGGACGAGCGTGGGCC 400
51 LeuLysAlaIleGluAlaLeuSerGlyLysIleGluLeuHisGlyLysPr 67
401 CTCAGGCCATCGAGGCGCTTTCAGGTAAATAGAACTGCACGGGAACC 450
67 oLeGluValGluHisSerValProLysArgGlnArgIleArgLysLeuG 84
451 CATAGAAAGTTGAGCACCTCGGTCCCAAAAGGCAAAAGGATTCGGAAACTTC 500
84 nIleArgAsnIleProProHisLeuGlnTrpGluValLeuAspSerLeu 100
501 AGATACCAAAATATCCCGCCCTCATTTACAGTCCGAGGTGCTGGATAGTTA 550
101 LeuValGlnThrGlyValValGluSerCysGluGlnValAsnThrAspSe 117
551 CTAGTCCAGTATGGAGTGGGAGAGCTGTGACCAAGTGAACACTGACTC 600
117 rGluThrAlaValValAsnValThrThrSerSerLysAspGlnAlaArgG 134
601 GGAACCTGCAGTTGTAATGTAACTTATCCAGTAAAGACCAAGCTAGAC 650
134 nAlaLeuAspLysLeuAsnGlyPheGlnLeuGluAsnPheThrLeuLys 150
651 AAGCAGTACAGCAAACTCAATCGATTTCAGTTAGAGAAATTCACCTTGAAA 700
151 ValAlaThrIleProAspGluMetAlaAlaGlnGlnAsnProLeuGlnG 167
701 GTAGCCTATATCCCTGATGAAATGGCCGCCAGCAAAACCCCTTGCAGCA 750
167 nProArgGlyArgArgGlyLeuGlyGlnArgGlySerSerArgGlnGlyS 184
751 GCCCGAGGTGCGCGGGGCTTGGGCGAGAGGGGCTCCTCAAGGACAGGGT 800
184 erProGlySerValSerLysGlnLysProCysAspLeuProLeuArgLeu 200
801 CTCAGGATCCGATCCCAAGCAGCAAAACCATGTGATTTGCCTCTCGCCTG 850
201 LeuValProThrGlnPheValGlyAlaIleIleGlyLysGluGlyAlaTh 217
851 CTGGTTCACCCCAANTTTGTTGGAGGCCATCATAGGAAAGAGGTGCCAC 900

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217 rIleArgAsnIleThrLysGlnThrGlnSerLysIleAspValHisArgL 234
901 CATTCGGAACATCACCAACAGACCCAGTCTAAAATCGATGTCCACCGTA 950
234 ySGluAsnAlaGlyAlaAlaGluLysSerIleThrIleLeuSerThrPro 250
951 AAGAAAATCGGGGCTGCTGAGAAATCGATTTACTATCTCTCTACTCCT 1000
251 GluGlyThrSerAlaAlaCysLysSerIleLeuGluIleMetHisLysG 267
1001 GAAGGCACCTCTCGGCTTGTAGTCTATTCTGGAGATTATGCATAAGGA 1050
267 uAlaGlnAspIleLysPheThrGluGluIleProLeuLysIleLeuAlaH 284
1051 AGCTCAAGATATAAAATTCACAGAAGAGATCCCTTGAAGATTTTAGTCT 1100
284 iAsnAsnPheValGlyArgLeuIleGlyLysGluGlyArgAsnLeuLys 300
1101 ATAATAACTTTGTTGGACGCTTATTGTTAAAGAAAGGAAATCTTAAA 1150
301 LysIleGluGlnAspThrAspThrLysIleThrIleSerProLeuGlnG 317
1151 AAATTGAGCAAGACACAGACACTAAATCACGATATCTCCATTGCAGGA 1200
317 uLeuThrLeuTyrAsnProGluArgThrIleThrValLysGlyAsnValG 334
1201 ATTCACGCTGTATAATCCAGAAGCAGCTATTACAGTTAAAGGCAATCTTG 1250
334 luThrCysAlaLysAlaGluGluGluIleMetLysLysIleArgGluSer 350
1251 AGACATGTGCCAAAGCTGAGGAGGAGATCATGAAGAAATCAGGGAGTCT 1300
351 TyrGluAsnAspIleAlaSerMetAsnLeuGlnAlaHisLeuIleProG 367
1301 TATGAAATGATATTGCTTCTATGAATCTTCAAGCACATTTAATTCCTGG 1350
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384 rProThrSerGlyProProSerAlaMetThrProProThrProGlnPhe 400
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1451 GAGCAATCAGAAACGGAGACTGTTTCATCAGTTTATCCAGCTCTATCAGT 1500
417 lGlyAlaIleIleGlyLysGlnGlyGlnHisIleLysGlnLeuSerArgp 434
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434 heAlaGlyAlaSerIleLysIleAlaProAlaGluAlaProAspAlaLys 450
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451 ValArgMetValIleIleThrGlyProProGluAlaGlnPheLysAlaG 467
1601 GTGAGGATGGTGATTATACCTGGACCCAGAGGCTCAGTTCAAGGCTCA 1650
467 nGlyArgIleThrGlyLysIleLysGluAsnPheValSerProLysG 484
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484 luGluValLysLeuGluAlaHisIleArgValProSerPheAlaAlaGly 500
1701 AAGAGGTGAACCTTGAAGCTCATATCAGAGTGCCATCCTTTGCTGCTGGC 1750
501 ArgValIleGlyLysGlyLysThrValAsnGlnLeuGlnAsnLeuSe 517
1751 AGGTTATTGAAAAGGAGGCAAAACGGTGAATGAACCTTCAGAAATTTGTC 1800

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1801 AAGTCGAGAGTGTGTTCCTCGTCACGACACACCTGATGAGATGACC 1850
534 lnValValValLysIleThrGlyHisPheTyrAlaCysGlnValAlaGln 550
1851 AAGTGGTTGTCAAATAACTGGTCACTTCTATGCTTGCAGGTGCCCCAG 1900
551 ArgLysIleGlnGlnLueLeuThrGlnValLysGlnHisGlnGlnGlnly 567
1901 AGAAAAATTCAGGAAATTCGACTCAGGTAAAGCAGCAGCAACACAGAA 1950
567 sAlaLeuGlnSerGlyProProGlnSerArgArgLys 579
1951 GGCCTCTGCAAGTGGACCACTCAGTCAAGACGGAAG 1987
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; Sequence 175, Application US/09630940B
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630,940B
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 175
; LENGTH: 4181
; TYPE: DNA
; ORGANISM: Homo sapiens
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Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-466-396A-176 x US-09-630-940B-175
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Align seg 1/1 to: US-09-630-940B-175 from: 1 to: 4181

1 MetAsnLysLeuTyrIleGlyAsnLeuSerGluAsnAlaAalaproSerAs 17
251 ATGAACAACACTGTATATCGGAACCTCAGCAGAGACGCCGCCCTCGGA 300
17 pLeuGluSerIlePheLysAspAlaLysIleProValSerGlyProPheL 34
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34 euValLysThrGlyTyrAlaPheValAspCysProAspGluSerTrpAla 50
351 TGGTGAAGACTGGCTGACGCTTCGGTGGACTGCCGGACGAGAGCTGGGCC 400
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401 CTCAGGCGCATCGAGCGCTTTTCAGGTAAATAGAACTGCACGGGAAACC 450
67 OtIleGluValGluHisSerValProLysArgGlnArgIleArgLysLeuG 84
451 CATAGAAGTTGAGCACTCGTCCCAAAAGGCAAGGATTCGGAACCTTC 500
84 InIleArgAsnIleProProHisLeuGlnTrpGluValLeuAspSerLeu 100
501 AGATACGAAATATCCCGCTCATTTACAGTGGGAGGTGCTGGATAGTTTA 550
101 LeuValGlnTyrGlyValValGluSerCysGlnValInValAsnThrAspSe 117
551 CTAGTCCAGTATGGAGTGGTGAGAGCTGTGAGCAAGTGAACACTGACTC 600
117 rGluThrAlaValValAsnValThrTyrSerSerLysAspGlnAlaArgG 134
601 GGAAACTGCAGTTGTAATGTAACTATTTCCAGTAAGGACCAAGCTAGAC 650
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; Sequence 175, Application US/09643597

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Liqun

; APPLICANT: Kalos, Michael D.

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Hosken, Nancy

; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Henderson, Robert A.

; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.455C11

; CURRENT APPLICATION NUMBER: US/09/643,597

; NUMBER OF SEQ ID NOS: 369

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 175

; LENGTH: 4181

; TYPE: DNA

; ORGANISM: Homo sapiens

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; NAME/KEY: unsure
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; OTHER INFORMATION: n=A,T,C or G
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US-09-643-597-175

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## alignment\_scores:

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Quality: 2956.00      Length: 579
Ratio: 5.105          Gaps: 0
Percent Similarity: 100.000      Percent Identity: 100.000

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## alignment\_block:

US-09-466-396a-176 x US-09-643-597-175

Align seg 1/1 to: US-09-643-597-175 from: 1 to: 4181

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251 ATGAACAACTGTATATCGGAACCTCAGCGAGACGCCGCCCTCGGA 300
17 pLeuGluSerIlePheLysAspAlaLysIleProValSerGlyProPheL 34
301 CCTAGAAGTATCTTCAGGACGCCAAGATCCGGTGTGCGGACCTTCC 350
34 euValLysThrGlyTyrAlaPheValAspCysProAspGluSerTrpAla 50
351 TGGTGAAGACTGGCTACCGCTTCCGCTGCTGCTGCTGCTGCTGCTG 400
51 LeuLysAlaIleGluAlaLeuSerGlyLysIleGluLeuHisGlyLysPr 67
401 CTCACGCCCATCGAGCGCTTTCAGGTAATAAGTAACTGCACGGGAACC 450
67 oileGluValGluHisSerValProLysArgGlnArgIleArgLysLeuG 84
451 CATAGAAGTTGAGCACTCGGTCCCAAAAAGGCAAGAGTTCGGAACCTC 500
84 lnIleArgAsnIleProProHisLeuGlnTrpGluValLeuAspSerLeu 100
501 AGATACGAATAATCCCGCTCATTTACAGTGGGAGGTGCTGGATGTTA 550
101 LeuValGlnTyrGlyValValGluSerCysGluGlnValAsnThrAspSe 117
551 CTAGTCCAGTATGGAGTGTGGAGAGCTGTGAGCAAGTGAACACTGACTC 600
117 rGluThrAlaValAlaAsnValThrTyrSerSerLysAspGlnAlaArgG 134
601 GGNAACTGCAGTTGTAAATGTAACTATTCCAGTAGGACCAAGCTAGAC 650

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151 ValAlaTyrIleProAspGluMetAlaAlaGlnGlnAsnProLeuGlnG 167
701 GTAGCCTATATCCCTGATGAATGGCCGCCAGCAAAACCCCTTGCAGCA 750
167 nProArgGlyArgGlyLeuGlyGlnArgGlySerSerArgGlnGlyS 184
751 GCCCGAGGTGCGCGGGGCTTGGCGAGAGGGCTCTCAAGCAGGGGT 800
184 erProGlySerValSerLysGlnLysProCysAspLeuProLeuArgLeu 200
801 CTCAGGATCCGTATCCAAAGCAGAAACCATGTGATTTGCTCTGCGCCTC 850
201 LeuValProThrGlnPheValGlyAlaIleIleGlyLysGluGlyAlaTh 217
851 CTGGTTCCCAACCAATTTGTTGGAGCCATCATAGGAAAAGAGGTGCCAC 900
217 rIleArgAsnIleThrLysGlnThrGlnSerLysIleAspValHisArgL 234
901 CATTCGGAACATCACCAACAGACCCAGCTAAATCGATGTCACCGTA 950
234 ysGluAsnAlaGlyAlaAlaGluLysSerIleThrIleLeuSerThrPro 250
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334 luThrCysAlaLysAlaGluGluIleMetLysLysIleArgGluSer 350
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351 TyrGluAsnAspIleAlaSerMetAsnLeuGlnAlaHisLeuIleProG 367
1301 TATGAAATGATATTGCTTCTATGAATCTTCAAGCACATTTAATCTCTG 1350
367 yLeuAsnLeuAsnAlaLeuGlyLeuPheProThrSerGlyMetProp 384
1351 ATTAATCTGAAGCGCTTGGGTCTGTCCACCCTTCCAGGGATGCCAC 1400
384 roProThrSerGlyProProSerAlaMetThrProProTyrProGlnPhe 400
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401 GluGlnSerGluThrGluThrValHisGlnPheIleProAlaLeuSerVa 417
1451 GAGCAATCAGAAACGGAGACTGTTTCATCATGTTATCCAGCTCTATCAGT 1500
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1501 CGGTGCCATCATCGCAACGAGGGCCAGCACATCAAGCAGCTTCTCTCGCT 1550

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1551 TTGCTGGAGCTTCAATAGATTGCTCCAGCGGAAGCAGATGCTAA 1600
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451 ValArgMetValIleIleThrGlyProGluAlaGlnPheLysAlaG1 467
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551 ArgLysIleGlnIleLeuThrGlnValLysGlnHisGlnGlnGly 567
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; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C12
; CURRENT APPLICATION NUMBER: US/09/662,786
; CURRENT FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 175
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; ORGANISM: Homo sapiens
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51 LeuLysAlaIleGluAlaLeuSerGlyLysIleGluLeuHisGlyLysPr 67
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167 nProArgGlyArgArgGlyLeuGlyGlnArgGlySerSerArgGlnGly 184
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; Sequence 175, Application US/09685696
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C13
; CURRENT APPLICATION NUMBER: US/09/685,696
; CURRENT FILING DATE: 2000-10-09
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 175
; LENGTH: 4181
; TYPE: DNA
; ORGANISM: Homo sapiens
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  Ratio: 5.105          Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

alignment_block:
US-09-466-396A-176 x US-09-685-696-175
Align seg 1/1 to: US-09-685-696-175 from: 1 to: 4181

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251 ATGAACAAACGTATATCGGAAACCTCAGGAGACGCCGCCCTCGGA 300
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17 pLeuGluSerIlePheLysAspAlaLysIleProValSerGlyProPheL 34
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301 CCTAGAAAGTATCTTCAAGGACGCCAAGATCCCGGTGTGCGGACCTTC 350
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34 euValLysThrGlyTyrAlaPheValAspCysProAspGluSerTrpAla 50
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517 rSerAlaGluValValProArgAspGlnThrProAspGluAsnAspG 534  
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1801 AGTCGAGAAATTTGTTCCCTCGTGACGACGACCTGATGGAATGACC 1850  
534 InValValLysIleThrGlyHisPheTyAlaCysGlnValAlaGln 550  
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551 ArgLysIleGlnGluIleLeuThrGlnValLysGlnHisGlnGlnIly 567  
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1901 AGAAAAATTCAGGAAATTTCTACTCAGGTAAGCAGCACCACCAACAGAA 1950  
567 saAlaLeuGlnSerGlyProProGlnSerArgArgLys 579  
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1951 GGCTCTGCAAGTGAACCACTCACTCAGACGGGAAG 1987

seq\_name: /cgn2\_6/ptodata/2/pna/us097b\_comb.seq:us-09-735-705-175

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: Sequence 175, Application US/09735705

: GENERAL INFORMATION:

: APPLICANT: Wang, Tongtong

: APPLICANT: Fan, Liqun

: APPLICANT: Kalos, Michael D.

: APPLICANT: Bangur, Chaitanya S.

: APPLICANT: Hosken, Nancy

: APPLICANT: Fanger, Gary R.

: APPLICANT: Li, Samuel X.

: APPLICANT: Wang, Aijun

: APPLICANT: Skeiky, Yasir A.W.

: APPLICANT: Henderson, Robert A.

: APPLICANT: McNeill, Patricia D.

: APPLICANT: Fanger, Neil

: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

: FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

: FILE REFERENCE: 210121.455C14

: CURRENT APPLICATION NUMBER: US/09/735,705

: CURRENT FILING DATE: 2000-12-12

: NUMBER OF SEQ ID NOS: 419

: SOFTWARE: FastSeq for Windows Version 3.0

: SEQ ID NO 175

: LENGTH: 4181

: TYPE: DNA

: ORGANISM: Homo sapiens

: FEATURE:

: NAME/KEY: unsure

: LOCATION: (3347)

: OTHER INFORMATION: n=A,T,C or G

: NAME/KEY: unsure

: LOCATION: (3502)

: OTHER INFORMATION: n=A,T,C or G

: NAME/KEY: unsure

: LOCATION: (3506)

: OTHER INFORMATION: n=A,T,C or G

: NAME/KEY: unsure

: LOCATION: (3520)

: OTHER INFORMATION: n=A,T,C or G

: NAME/KEY: unsure

: LOCATION: (3538)

: OTHER INFORMATION: n=A,T,C or G

: NAME/KEY: unsure

: LOCATION: (3646)

: OTHER INFORMATION: n=A,T,C or G

: NAME/KEY: unsure

: LOCATION: (3940)

: OTHER INFORMATION: n=A,T,C or G

: NAME/KEY: unsure

: LOCATION: (3968)

: OTHER INFORMATION: n=A,T,C or G

: NAME/KEY: unsure

: LOCATION: (3974)

: OTHER INFORMATION: n=A,T,C or G

: NAME/KEY: unsure

: LOCATION: (4036)

: OTHER INFORMATION: n=A,T,C or G

: NAME/KEY: unsure

: LOCATION: (4056)

: OTHER INFORMATION: n=A,T,C or G

: NAME/KEY: unsure

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: OTHER INFORMATION: n=A,T,C or G

: NAME/KEY: unsure

: LOCATION: (4080)

: OTHER INFORMATION: n=A,T,C or G

: NAME/KEY: unsure

: LOCATION: (4088)

: OTHER INFORMATION: n=A,T,C or G

: NAME/KEY: unsure

: LOCATION: (4115)

: OTHER INFORMATION: n=A,T,C or G

: US-09-735-705-175

alignment\_scores:

Quality: 2956.00 Length: 579

Ratio: 5.105 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block:

US-09-466-396A-176 x US-09-735-705-175 ..

Align seg 1/1 to: US-09-735-705-175 from: 1 to: 4181



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17 pLeuGluSerIlePheLysAspAlaLysIleProValSerGlyProPheL 34
301 CCTAGAAAGTATCTTCAAGGACGCCAAGATCCCGGTGTCGGGACCTTCC 350
34 euValLysThrGlyTyrAlaPheValAspCysProAspGluSerTrpAla 50
351 TGTGTAAGACTGGCTACGGCTTCGTGGACTGCCCGGACGAGAGCTGGCC 400
51 LeuLysAlaIleGluAlaLeuSerGlyLysIleGluLeuHisGlyLysPr 67
401 CTCAGGCCATCCAGCGCTTTCAGGTAAATAAGAACTGCACGGGAACC 450
67 oileGluValGluHisSerValProLysArgGlnArgIleArgLysLeuG 84
451 CATAGAAGTTGACACTCGCTGCCAAAAGGCAAGGATTCGGAACCTTC 500
84 lnIleArgAsnIleProProHisLeuGlnTrpGluValLeuAspSerLeu 100
501 AGATACGAATAATCCCGCTCATTTACAGTGGGAGGTGCTGGATAGTTTA 550
101 LeuValGlnTyrGlyValValGluSerCysGluGlnValAsnThrAspSe 117
551 CTAGTCCAGTATCGAGTGGTGGAGACTGTGAGCAAGTAAGCACTGACTC 600
117 rGluThrAlaValAlaValAsnValThrTyrSerSerLysAspGlnAlaArg 134
601 GGAACCTGACGTTGTAATGTACCTATTCCAGTAAGGACCAAGCTAGAC 650
134 lnAlaLeuAspLysLeuAsnGlyPheGlnLeuGluAsnPheThrLeuLys 150
651 AAGCACTAGACAAACTGAATGGATTTTCAGTTAGAGAAATTCACCTTGAA 700
151 ValAlaTyrIleProAspGluMetAlaAlaGlnGlnAsnProLeuGlnGl 167
701 GTAGCTATATCCCTGATGAATGGCGGCCAGCAAAACCCCTTGCAGCA 750
167 nProArgGlyArgArgGlyLeuGlyGlnArgGlySerSerArgGlnGlys 184
751 GCCCGAGGTCGCCGGGGCTTGGGACAGAGGGCTCTCAAGGCAGGGGT 800
184 erProGlySerValSerLysGlnLysProCysAspLeuProLeuArgLeu 200
801 CTCAGGATCCGTATCCAAGCAGAAACCATGTGATTTGCCCTCTGCGCCTG 850
201 LeuValProThrGlnPheValGlyAlaIleIleGlyLysGluGlyAlaTh 217
851 CTGGTTCCCAACCAANTTGTGGAGCCATCATAGGAAAAGAGAGTGCAC 900
217 rIleArgAsnIleThrLysGlnThrGlnSerLysIleAspValHisArgL 234
901 CATTGGGAACATCACCACAGACCCAGCTCTAAATCGATGTCCACCGTA 950
234 ySGluAsnAlaGlyAlaAlaGluLysSerIleThrIleLeuSerThrPro 250
951 AAGAAAATCGGGGCTGCTGAGAAGTCGATTACTATCCCTCTCTACTCCT 1000
251 GluGlyThrSerAlaAlaCysLysSerIleLeuGluIleMetHisLysGl 267
1001 GAAGGCACCTCTCGGCTTGAAGTCTATTCTGGAGATTATGCATAAGGA 1050
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1051 AGCTCAGATATATAAATTCAGAAGAGATCCCTTGAAGATTTTGAAGTCT 1100
284 isAsnAsnPheValGlyArgLeuIleGlyLysGluGlyArgAsnLeuLys 300
1101 ATAATACTTTGTGGAGCTTATTGGTAAAGAGGAAGAAATCTTAA 1150
301 LysIleGluGlnAspThrAspThrLysIleThrIleSerProLeuGlnGl 317
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1151 AAAATTGAGCAAGACACAGACTAAATAACCATATCTCATTTGCAGGA 1200
317 uLeuThrLeuTyrAsnProGluArgThrIleThrValLysGlyAsnValG 334
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334 luThrCysAlaLysAlaGluGluGluMetLysLysIleArgGluSer 350
1251 AGACATGTGCCAAAGCTGAGGAGGAGATCATGAAGAAAATCAGGGAGTCT 1300
351 TyrGluAsnAspIleAlaSerMetAsnLeuGlnAlaHisLeuIleProGl 367
1301 TATGAAATGATATGCTTCTATGAATCTTCAAGCACATTTAATTCCTGG 1350
367 yLeuAsnLeuAsnAlaLeuGlyLeuPheProProThrSerGlyMetProp 384
1351 ATTTAAATCTGAACGCCCTTGGGTCTGTTCACCACCTTCAGGGATGCCAC 1400
384 roProThrSerGlyProProSerAlaMetThrProProTyrProGlnPhe 400
1401 CTCGCCACTCAGGGCCCTTCAGCCATGACTCTCTCCTACCCGCACTTT 1450
401 GluGlnSerGluThrGluThrValHisGlnPheIleProAlaLeuSerVa 417
1451 GAGCAATTCAGAAACGGAGACTGTTCATCAGTTTATCCACGCTCTATCAGT 1500
417 lGlyAlaIleIleGlyLysGlnGlyGlnHisIleLysGlnLeuSerArgP 434
1501 CGGTGCCATCATCGGCAAGCGGCGCCAGCACATCAAGCAGCTTTCGCT 1550
434 heAlaGlyAlaSerIleLysIleAlaProAlaGluAlaProAspAlaLys 450
1551 TTGCTGGAGCTTCAATTAAGATTGCTCCAGCGGAAGCACCAGATGCTAAA 1600
451 ValArgMetValIleIleThrGlyProProGluAlaGlnPheLysAlaGl 467
1601 GTGAGGATGTTGATTATCTGTCGACCCAGAGGCTCAGTTCAAGGCTCA 1650
467 nGlyArgIleTyrGlyLysIleLysGluGluAsnPheValSerProLysG 484
1651 GGAAGAAATTTATGGAATAATTAAGAAAGAAACTTTGTAGTCTCTAAG 1700
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517 rSerAlaGluValValProArgAspGlnThrProAspGluAsnAspG 534
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1851 AAGTGGTTGTCAAAATAACTGGTGCATCTATGCTTGCCAGGTGCCCAG 1900
551 ArgLysIleGlnGluIleLeuThrGlnValLysGlnHisGlnGlnLys 567
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; Sequence 175, Application US/09850716
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
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APPLICANT: Fan, Liqun  
APPLICANT: Kalos, Michael D.  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Hosken, Nancy  
APPLICANT: Fanger, Gary R.  
APPLICANT: Li, Samuel X.  
APPLICANT: Wang, Aijun  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Henderson, Robert A.  
APPLICANT: McNeill, Patricia D.  
APPLICANT: Fanger, Neil  
APPLICANT: Retter, Marc W.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
FILE REFERENCE: 210121.455C15  
CURRENT APPLICATION NUMBER: US/09/850,716  
CURRENT FILING DATE: 2001-05-07  
NUMBER OF SEQ ID NOS: 440  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 175  
LENGTH: 4181  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (3347)  
OTHER INFORMATION: n=A,T,C or G  
NAME/KEY: unsure  
LOCATION: (3502)  
OTHER INFORMATION: n=A,T,C or G  
NAME/KEY: unsure  
LOCATION: (3506)  
OTHER INFORMATION: n=A,T,C or G  
NAME/KEY: unsure  
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NAME/KEY: unsure  
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OTHER INFORMATION: n=A,T,C or G  
NAME/KEY: unsure  
LOCATION: (4115)  
OTHER INFORMATION: n=A,T,C or G  
US-09-850-716-175

## alignment\_scores:

Quality: 2956.00 Length: 579  
Ratio: 5.105 Gaps: 0  
Percent Similarity: 100.000 Percent Identity: 100.000

## alignment\_block:

US-09-466-396A-176 x US-09-850-716-175

Align seg 1/1 to: US-09-850-716-175 from: 1 to: 4181

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301 CCTAGAAAGTATCTTCAAGGACGCCCAAGATCCCGGTGTCGGGACCTTCC 350  
34 euValLysThrGlyTyrAlaPheValAspCysProAspGluSerTrpAla 50  
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351 TGGTGAAGACTGGCTACGCGTTCTGTGGACTGCCCGGACGAGAGCTGGGCC 400  
51 LeuLysAlaIleGluAlaLeuSerGlyLysIleGluLeuHisGlyLysPr 67  
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401 CTCAGGGCCATCGAGCGCGTTTCAGGTAAATAGAACTGCACGGGAAACC 450  
67 oileGluValGluHisSerValProLysArgGlnArgIleArgLysLeuG 84  
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451 CATAGAAGTTGAGCACTCGGTCCCAAAAGGCAAGGATTCGGAACATTC 500  
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117 rGluThrAlaValValAsnValThrTyrSerSerLysAspGlnAlaArgG 134  
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167 nProArgGlyArgArgGlyLeuGlyGlnArgLysSerSerArgGlnGlys 184  
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284 iAsnAsnPhelValGlyArgLeuIleGlyLysGluGlyArgAsnLeuLys 300
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301 LysIleGluGlnAspThrAspThrLysIleThrIleSerProLeuGlnG 317
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351 TyrGluAsnAspIleAlaSerMetAsnLeuGlnAlaHisIleProG 367
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1301 TATGAAATGATATTGCTTCTATGAATCTTCAAGCACATTTAATTCCTGG 1350
367 yLeuAsnLeuAsnAlaLeuGlyLeuPheProThrSerGlyMetProP 384
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1351 ATTTAATCTGAAGCCCTTGGGCTGTTCACCCACCCTTCAGGGATGCCAC 1400
384 roProThrSerGlyProProSerAlaMetThrProProTyrProGlnPhe 400
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1401 CTCCACCTCAGGGCCCTCTCAGCCATGACTCTCCCTACCGCAGTTT 1450
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417 lGlyAlaIleGlyLysGlnGlyGlnHisIleLysGlnLeuSerArgP 434
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517 rSerAlaGluValValProArgAspGlnThrProAspGluAsnAspG 534
1801 AAGTGACAGAAGTTGTTGCTCCTCGTCCAGCAGACCTGATGAGAATGACC 1850
534 lnValValValLysIleThrGlyHisPheTyrAlaCysGlnValAlaGln 550
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551 ArgLysIleGlnGluIleLeuThrGlnValLysGlnHisGlnGlnGlnLy
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567 sAlaLeuGlnSerGlyProGlnSerArgArgLys 579
1951 GGCTCTGCAAGTGGACCACTCAGTCAAGACGGAAG 1987
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seq\_documentation\_block:

; Sequence 145, Application US/60281593

; GENERAL INFORMATION:

; APPLICANT: Amy Lasek

; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER

; FILE REFERENCE: PA-0045 P

; CURRENT APPLICATION NUMBER: US/60/281.593

; CURRENT FILING DATE: 2001-04-04

; NUMBER OF SEQ ID NOS: 519

; SOFTWARE: PERL Program

; SEQ ID NO 145

; LENGTH: 4434

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; OTHER INFORMATION: Incyte ID No: 1383415.3

; NAME/KEY: unsure

; LOCATION: 2203

; OTHER INFORMATION: a, t, c, g, or other

; US-60-281-593-145

alignment\_scores:

Quality: 2945.00

Ratio: 5.095

Percent Similarity: 99.827

Percent Identity: 99.655

alignment\_block:

US-09-466-396A-176 x US-60-281-593-145

Align seg 1/1 to: US-60-281-593-145 from: 1 to: 4434

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302 CCTAGAAAGTATCTTCAAGGACGCCAAGATCCCGGTGTCGGGACCTTCC 351
34 euValLysThrGlyTyrAlaPheValAspCysProAspGluSerTrpAla 50
352 TGGTGAAGACTGGCTACGCGTTGCTGGACTGCCCGGACGAGAGCTGGCC 401
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552 CTAGTCCAGTATCGAGTGTGGAGAGCTGTGACCAAGTGAACACTCACTC 601
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602 GGAACCTGCAGTTGTAATGTAACTTATCCAGTAAGACCAAGCTAGAC 651
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251 GluGlyThrSerAlaAlaCysLysSerIleLeuGluIleMetHisLysG 267
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301 LysIleGluGlnAspThrAspThrLysIleThrIleSerProLeuGlnG 317
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; Sequence 347, Application US/09542615A  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy A.  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY  
; FILE REFERENCE: 210121.455C8  
; CURRENT APPLICATION NUMBER: US/09/542,615A  
; CURRENT FILING DATE: 2000-04-14  
; NUMBER OF SEQ ID NOS: 350  
; SOFTWARE: FastSeq for Windows Version 3.0  
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; LENGTH: 1740  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-542-615A-347

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1151	CTCCACCTCAGGGCCCTTACGCCATGACTCTCTCCCTACCCGAGTTT	1200
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; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chailanya S.
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; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; OF LUNG CANCER  
; FILE REFERENCE: 210121.455C9  
; CURRENT APPLICATION NUMBER: US/09/606, 421A  
; CURRENT FILING DATE: 2000-06-28  
; NUMBER OF SEQ ID NOS: 354  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 347  
; LENGTH: 1740  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-606-421A-347

## alignment\_scores:

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Ratio: 5.101 Gaps: 0  
Percent Similarity: 99.655 Percent Identity: 99.655

## alignment\_block:

US-09-466-396A-176 x US-09-606-421A-347

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51 CCTAGAAAGTATCTCAAGAGCCCAAGATCCCGGTGTCGGACCTTC 100  
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Date: Sep 29, 2001 3:43 PM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

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; Sequence 175, Application US/09510376A  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tonglong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Hosken, Nancy A.  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Fanger, Gary R.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY  
; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C7  
; CURRENT APPLICATION NUMBER: US/09/510,376A  
; CURRENT FILING DATE: 2001-08-21  
; NUMBER OF SEQ ID NOS: 330  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 175  
; LENGTH: 4181  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (1)-(4181)  
; OTHER INFORMATION: n=A,T,C or G  
US-09-510-376A-175

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34 euVallysThrGlyTyrAlaPheValAspCysProAspGluSerTirpAla 50  
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; Sequence 21954, Application PC/TUS0108631  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-049  
; CURRENT APPLICATION NUMBER: PCT/US01/08631  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 21954  
; LENGTH: 4264  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIMILAR  
; LOCATION: (1774)..(2013)  
; OTHER INFORMATION: 55% homologous to Homo sapiens IGF-II mRNA-binding protein  
; OTHER INFORMATION: 3, accession number AF117108, Smith-Waterman Score=204.  
PCT-US01-08631-21954

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seq\_documentation\_block:

; Sequence 12583, Application PC/TUS0108631

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc

; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

; FILE REFERENCE: 21272-049

; CURRENT APPLICATION NUMBER: PCT/US01/08631

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: 09/540,217

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: 09/649,167

; PRIOR FILING DATE: 2000-08-23

; NUMBER OF SEQ ID NOS: 60736

; SOFTWARE: Custom

; SEQ ID NO 12583

; LENGTH: 1985

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SIMILAR

; LOCATION: (164)..(3)

; OTHER INFORMATION: 79% homologous to Homo sapiens Human secreted protein

; OTHER INFORMATION: HLYES38, SEQ ID NO:220, accession number Y86305, Smith-Waterman Sc

; OTHER INFORMATION: -211.

PCT-US01-08631-12583

alignment\_scores:

Quality: 2675.00 Length: 584

Ratio: 4.785 Gaps: 4

Percent Similarity: 95.719 Percent Identity: 92.295

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34 euValLysThrClyTyrAlaPheValaspCysProAspGluSerTrpAla 50

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51 LeuLysAlaIleGluAlaLeuSerGlyLysIleGluLeuHisGlyLysPr 67

151 CTCACAGGCCATTGAGCGCTTTCAGTAAATAGAACTGCACGGGAACC 200

67 oileGluValGluHuHisSerValProLysArgGlnArgIleArgLysLeu 84

201 CATAGAAGTTGAGCACTCGGTCCCAAAAGGCAAGGATTCGGAACCTC 250

84 InIleArgAsnIleProHisLeuGlnTTPGluValLeuAspSerLeu 100

251 AGATACGAAATATCCCTCCTCCTACAGTGGAGGTGCTGGATAGTTGA 300

101 LeuValGlnTyrGlyValValGluSerCysGluGlnValAsnThrAspSe 117

301 CTAGTCCAGTATGAGTGGTGGAGAGCTGTTCAGCAAGTGAACACTGACTC 350

117 rGluThrAlaValValAsnValThrTyrSerSerLysAsp.....G 131

351 GGAACACTGCAGTTGTAAATGTAACTATTCAGTAAGGACCAAGCTAGAC 400

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147 heThrLeuLysValAlaTyrIleProAspGluMetAlaAlaGlnGlnAsn 163

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701 TGTCCACCGTAAAGAAAATGCGAGGGCTGCTCAGAAAGTCGATTACTATCC 750

247 euSerThrProGluGlyThrSerAlaAlaCysLysSerIleLeuGluIle 263

751 TCTCTACTCTGGAAGGCACCTCTCGCGCTTGAAGTCTATTCTGGAGATT 800

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851 GATTTTAGCTCAAAATAACTTGTGGCGCTTATTGTTAAAGAAGGAA 900

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530 spGluAsnAspGlnValValValLysIleThrGlyHisPheTyrAlaCys 546
1598 ATCAGATGACCAAGTGGTGTCAAAATAACTGCTCATTCTATGCTTGC 1647
547 GlnValAlaGlnArgLysIleGlnGluIleLeuThrGlnValLysGlnHI 563
1648 CAGGTTGCCAGAGAAAAATTCAGGAAATTTCTGACTCAGGTAAGCAGCA 1697
563 sGlnGlnGlnLysAlaLeuGlnSerGlyProProGlnSerArgArgLys 579
1698 CCAACAACAGAGAGGCTCTGCAAAATGGACCACCTCAGTCAAGACGGAAG 1746
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seq\_name: /cgn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq:pct-US01-08631-6785

seq\_documentation\_block:  
; Sequence 6785, Application PC/TUS0108631

; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-049  
; CURRENT APPLICATION NUMBER: PCT/US01/08631  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 6785  
; LENGTH: 2010  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIMILAR  
; LOCATION: (50)..(1843)  
; OTHER INFORMATION: 100% homologous to Homo sapiens IGF-II mRNA-binding protein  
; OTHER INFORMATION: 2,accession number AF117107,Smith-Waterman Score=3059.  
PCT-US01-08631-6785

alignment\_scores:  
Quality: 1950.50 Length: 591  
Ratio: 3.817 Gaps: 8  
Percent Similarity: 86.464 Percent Identity: 65.313

alignment\_block:

US-09-466-396a-176 x PCT-US01-08631-6785 ..

Align seq 1/1 to: PCT-US01-08631-6785 from: 1 to: 2010

1 MetAsnLysLeuTyrIleGlyAsnLeuSerGluAsnAlaProSerAs 17

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||||| 50 ATGAACAAGCTTTACATCGGGAACCTTGAGCCCGCGGTCCACGCCGACGA 99
||||| 17 pLeuGluSerIlePheLysAspAlaLysIleProValSerGlyProPhe 34
||||| 100 CCTCCGCGACTCTTTGGGACAGGAAGCTGCCCTGGCGGACAGGTCC 149
||||| 34 euValLysThrGlyTyrAlaPheValAspCysProAspGluSerTrpAla 50
||||| 150 TGTGTAAGTCCGCTAGCGCTTGTGAGTACCCCGACCAAGTGGGCTG 199
||||| 51 LeuLysAlaIleGluAlaLeuSerGlyLysIleGluLeuHisGlyLysPr 67
||||| 200 ATCCGCGCCATCGAGACCTCTCGGGTAAAGTGAATGTCATGGGAAAT 249
||||| 67 oIleGluValGluHisSerValProLysArgGlnArgIleArgLysLeuG 84
||||| 250 CATGGAAGTTGATTACTCAGTCTCTAAAGAGTAAAGGAGCAGGAAATTC 299
||||| 84 InIleArgAsnIleProProHisLeuGlnTrpGluValLeuAspSerLeu 100
||||| 300 AGATTGCAAAACATCCCTCCTCAGTGGAGGTGTTGGATGGACTT 349
||||| 101 LeuValGlnTyrGlyValValGluSerCysGluGlnValAsnThrAspSe 117
||||| 350 TTGGCTCAATATGGGACAGTGGAGATGTGGAACAAGTCAACACAGACAC 399
||||| 117 rGluThrAlaValValAsnValThrTyrSerSerLysAspGlnAlaArgG 134
||||| 400 AGAAGCCGCGTGTCAACGTCATATGCAACAAGAGAGAGAGCAAAA 449
||||| 134 InAlaLeuAspLysLeuAsnGlyPheGlnLeuGluAsnPheThrLeuLys 150
||||| 450 TAGCCATGGAGAGCTAAAGCGGCATCAGTTTGAGAACTACTCTCTTCAAG 499
||||| 151 ValAlaTyrIleProAspGluMetAlaAlaGlnGlnAsnProLeuGlnG1 167
||||| 500 ATTTCTTACATCCCGGATGAAGAGGTGAGCTCCCTTCGCCCTCAG.. 547
||||| 167 nProArgGlyArgArgGlyLeuGlyGlnArgGlySerSerArgGlnGly. 183
||||| 548 .....CGAGCCCGAGGT.....GGGACCACTCTTCCCGGAGCAAGGCC 587
||||| 184 ..SerProGlySerValSerLysGlnLysProCysAspLeuProLeuArg 199
||||| 588 ACGCCCTGGGGCAGCTTCTCAGGCCACAGACAGATTGATTTCCCGCTCGG 637
||||| 200 LeuLeuValProThrGlnPheValGlyAlaIleIleGlyLysGluGlyAl 216
||||| 638 ATCTGTGTCCTCCACCCAGTTTGTGTGGTGCATCATCGGAAAGGAGGCTT 687
||||| 216 aThrIleArgAsnIleThrLysGlnThrGlnSerLysIleAspValHisA 233
||||| 688 GACCATAAAGAACATCATCAAGCAGACCCAGTCCCGGTAGATATCCATA 737
||||| 233 rgLysGluAsnAlaGlyAlaAlaGlySerIleThrIleLeuSerThr 249
||||| 738 GAAAGAGAACTCTGGAGCTGCAGAGAAGCTGTCCACCATCCATGCCACC 787
||||| 250 ProGluGlyThrSerAlaAlaCysLysSerIleLeuGluIleMetHisLy 266
||||| 788 CCAGAGGGGACTTCTGAAGCATGCCGATGATTTGAAATCATGCAGAA 837
||||| 266 sGluAlaGlnAspIleLysPheThrGluGluIleProLeuLysIleLeuA 283
||||| 838 AGAGGCAGATGAGACCAAACTAGCCGAGAGAGATTCCTCTGNAATCTGG 887
||||| 283 laHisAsnAsnPheValGlyArgLeuIleGlyLysGluGlyArgAsnLeu 299
||||| 888 CACACAATGGCTTGGTGGAGACTGATTGGAAAAAGAGGAGCAAAATTG 937
||||| 300 LysLysIleGluGlnAspThrAspThrLysIleThrIleSerProLeuG1 316
|||||
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889 ATTCTCTACATCCCGGATGAGAGGTGAGCTCCCTTCGCCCTCAG... 936
167 nProArgGlyArgArgGlyLeuGlyGlnArgGlySerSerArgGlnGly. 183
937 ....CGAGCCAGCGT.....GGGACCACTCTTCCCGGAGAGGCC 976
184 ..SerProGlySerValSerLysGlnLysProCysAspLeuProLeuArg 199
977 ACCCCCTGGGGCAGCTCTCAGCCGACAGAGATTGATTCCTCCGCTGCCG 1026
200 LeuLeuValProThrGlnPheValGlyAlaIleIleGlyLysGlyAla 216
1027 ATCTGTGTCCCAACCAGATTGTGTGTGTCATCATCGAAAGAGGCTT 1076
216 aThrIleArgAsnIleThrLysGlnThrGlnSerLysIleAspValHis 233
1077 GACCATAAAGAACATCACTAAGCAGACCCAGTCCCGGTAGATATCCATA 1126
233 rLysGluAsnAlaGlyAlaAlaGluLysSerIleThrIleLeuSerThr 249
1127 GAAAGAGAACTCTGGAGCTGCAGAGAGCCTGTCCACCATCCAGCCACC 1176
250 ProGluGlyThrSerAlaAlaCysLysSerIleLeuGluIleMethIsty 266
1177 CCAGAGGGACTTCTGAAGCATCCCGCATGATCTTGAATCATGTCAGAA 1226
266 sGluAlaGlnAspIleLysPheThrGluGluIleProLeuLysIleLeu 283
1227 AGAGCAGATGAGACAAACTAGCCGAAGAGATTCTCTGAAATCTTGG 1276
283 laHisAsnAsnPheValGlyArgLeuIleGlyLysGluGlyArgAsnLeu 299
1277 CACACAATGGCTTGGTGGAGAGCTGATTGGAAAGAGGACAGAAATTTG 1326
300 LysLysIleGluGlnAspThrAspThrLysIleThrIleSerProLeuG 316
1327 AAGAAATGAAATGAACATGAACAGGACCAAGATACCAATCTCATCTTGA 1376
316 nGluLeuThrLeuThrAsnProGluArgThrIleThrValLysGlyAsnV 333
1377 GGATTTGAGCATATACAAACCGGAAAGAACCACTCACTGTGAAGGCCAC 1426
333 alGluThrCysAlaLysAlaGluGluIleMetLysLysIleArgGlu 349
1427 TTGAGGCCTGTCCAGTGTGAGATAGAGATTATGAAGAGCTGCCTGAG 1476
350 SerTyrGluAsnAspIleAlaSerMetAsnLeuGlnAlaHisLeuIlePr 366
1477 GCCTTTGAAATGATATGCTGGCTGTATACACCCACTCC..... 1515
366 oGlyLeuAsnLeuAsnAlaLeuGlyLeuPheProProThrSerGlyMetP 383
1516 .....GCATACTTC..... 1524
383 roProProThrSerGlyProProSerAlaMetThrProProThrProGln 399
1525 .....TCCAGCCTGTACCCCATCACAGTTTGGCCGCTTCCCGCAT 1566
400 PheGluGln...SerGluThrGluThrValHisGlnPheIleProAlaLe 415
1567 CATCACTCTTATCCAGAGAGAGATTGTGAATCTCTTCATCCCAACCCA 1616
415 uSerValGlyAlaIleIleGlyLysGlnGlyGlnHisIleLysGlnLeuS 432
1617 GGCTGTGGGGCCCATCATCGGAAGAAGGGGCACACATCAACAGCTGG 1666
432 erArgPheAlaGlyAlaSerIleLysIleAlaProAlaGluAlaProAsp 448
1667 CGAATTTCGGCGAGCTCTATCAAGATTGCCCTCGCGAAGGCCAGAC 1716
449 AlaLysValArgMetValIleIleThrGlyProProGluAlaGlnPheLy 465
1717 GTCAGGAAAGGATGGTCATCATCAGGGGCCACCGAAGCCAGTTCAA 1766
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465 sAlaGlnGlyArgIleTyrGlyLysLysLysGluGluAsnPheValSerP 482
1767 GGCCCGAGGACGATCTTTGGGAACTGAAAGAGGAAACTTCTTTAAAC 1816
482 rLysGluGluValLysLeuGluAlaHisIleArgValProSerPheAla 498
1817 CCAAAGAAGTGAAGCTGGAAGCGCATATCAGAGTGCCTCTTCCACA 1866
499 AlaGlyArgValIleGlyLysGlyGlyLysThrValAsnGluLeuGlnAs 515
1867 GCTGGCCGGGTGATTGGCAAGGTGGCAACCGTGAACCAACTGCAGAA 1916
515 nLeuSerSerAlaGluValValProArgAspGlnThrProAspGluA 532
1917 CTTAACCAAGTGCAGAGTCATCGTGCCTCGTACCAAAACCCAGATGAA 1966
532 snAspGlnValValValLysIleThrGlyHisPheTyrAlaCysGlnVal 548
1967 ATGAGGAAGTGCATCGTCAAGAAATTATCGGGCATTCTTTGTAGCCAG 2016
549 AlaGlnArgLysIleGlnGluIleLeuThrGlnValLysGlnHisGlnGl 565
2017 GCACAGCGCAAGATCAGGGAATTTGTACAACAGTGAACGAGCAGGAGCA 2066
565 nGln 566
2067 GAAA 2070
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seq\_name: /cgn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq:PCT-US01-08631-21952

seq\_documentation\_block:

; Sequence 21952, Application PC/TUS0108631

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc

; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

; FILE REFERENCE: 21272-049

; CURRENT APPLICATION NUMBER: PCT/US01/08631

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: 09/540,217

; PRIOR FILING DATE: 2000-03-31

; PRIOR APPLICATION NUMBER: 09/649,167

; PRIOR FILING DATE: 2000-08-23

; NUMBER OF SEQ ID NOS: 60736

; SOFTWARE: Custom

; SEQ ID NO 21952

; LENGTH: 1998

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SIMILAR

; LOCATION: (3)..(179)

; OTHER INFORMATION: 94% homologous to Homo sapiens IGF-II mRNA-binding protein

; OTHER INFORMATION: 3.accession number AF117108,Smith-Waterman Score=293.

PCT-US01-08631-21952

alignment\_scores:

Quality: 776.50

Ratio: 3.806

Percent Similarity: 36.691

Length: 556

Gaps: 3

Percent Identity: 34.712

alignment\_block:

US-09-466-396A-176 x PCT-US01-08631-21952

Align seg 1/1 to: PCT-US01-08631-21952 from: 1 to: 1998

24 AspAlaLysIleProValSerGlyProPheLeuValLysThrGlyTyrAl 40

|||||

3 GAGCCCAAGATCCCGTGTGGGACCCCTTCTTGTGAAGATTGGCTACGC 52

|||||

40 aPheValAspCysProAspGluSerTrpAlaLeuLysAlaIleGluAla 57

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|||||

53 GTTCGTGGACTCCAGACAGCATCTGGCCCTCAAGGCCATTGAGGCC 102  
57 euserGlyLysIleGluLeuHisGlyLysProIleGluValGluHisSer 73  
103 TTTTCAAGTAAATAGAACTGCACGGAAACCCATAGAAATTGAGCACTG 152  
74 ValProLysArgGlnArgIleArgLysLeuGlnIleArgAsnIleProPr 90  
153 GTCCCAAAAGCAAGGATTGGA ..... 176  
90 ohfLysGlnTrpGluValLeuAspSerLeuLeuValGlnTyrGlyValV 107  
176 ..... 176  
107 aigluserCysGluGlnValAsnThrAspSerGluThrAlaValValAsn 123  
176 ..... 176  
124 ValThrTyrSerSerLysAspGlnAlaArgGlnAlaLeuAspLysLeuAs 140  
176 ..... 176  
140 nGlyPheGlnLeuGluAsnPheThrLeuLysValAlaTyrIleProAspG 157  
176 ..... 176  
157 luMetAlaGlnGlnAsnProLeuGlnGlnProArgGlyArgArgGly 173  
176 ..... 176  
174 LeuGlyGlnArgGlySerSerArgGlnGlySerProGlySerValSerly 190  
176 ..... 176  
190 sGlnLysProCysAspLeuProLeuArgLeuLeuValProThrGlnPheV 207  
176 ..... 176  
207 alGlyAlaIleIleGlyLysGluGlyAlaThrIleArgAsnIleThrLys 223  
176 ..... 176  
224 GlnThrGlnSerLysIleAspValHisArgLysGluAsnAlaGlyAlaAl 240  
177 ..... GAAATGCGAGGGCTGC 193  
240 aGlyLysSerIleThrIleLeuSerThrProGluGlyThrSerAlaAlaC 257  
194 TGAGAAGTCGATTACTCTCTACTCTCTGAGGCACCTCTCGCGCTT 243  
257 ysLysSerIleLeuGluIleMetHisLysGluAlaGlnAspIleLysPhe 273  
244 GTAAGTCTATTCTGGAGATTATGCGTAAGGAACCTCAAGATGTAATTC 293  
274 ThrGluGluIleProLeuLysIleLeuAlaHisAsnAsnPheValGlyAr 290  
294 ACAGAAGAGATCCCTTG ..... 311  
290 gLeuIleGlyLysGluGlyArgAsnLeuLysLysIleGluGlnAspThrA 307  
311 ..... 311  
307 spThrLysIleThrIleSerProLeuGlnGluLeuThrLeuTyrAsnPro 323  
311 ..... 311  
324 GluArgThrIleThrValLysGlyAsnValGluThrCysAlaLysAlaGl 340  
311 ..... 311  
340 uGluGluIleMetLysLysIleArgGluSerTyrGluAsnAspIleAlas 357  
311 ..... 311

357 erMetAsnLeuGlnAlaHisLeuIleProGlyLeuAsnLeuAlaLeu 373  
311 ..... 311  
374 GlyLeuPheProThrSerGlyMetProProThrSerGlyProPr 390  
311 ..... 311  
390 oSerAlaMetThrProProTyrProGlnPheGluGlnSerGluThrGluT 407  
311 ..... 311  
407 hrValHisGlnPheIleProAlaLeuSerValGlyAlaIleIleGlyLys 423  
312 ..... TTTATCCGGCTCTATCAGTCAGAGCCCTCATCAGCAAG 350  
424 GlnGlyGlnHisIleLysGlnLeuSerArgPheAlaGlyAlaSerIleLy 440  
351 CAGGCCACACATCAAGCAGCTTTCTCGCTTGTGGAGCTTCAAGTAA 400  
440 sIleAlaProAlaGluAlaProAspAlaLysValArgMetValIleIleT 457  
401 GATTCTCCAGTGGAGGACCAGATGCTAAGGTGAGGATGTTGATGATCG 450  
457 hrGlyProProGluAlaGlnPheLysAlaGlnGlyArgIleTyrGlyLys 473  
451 CTGGATCACCAAGATTGT ..... 467  
474 IleLysGluGluAsnPheValSerProLysGluGluValLysLeuGluAl 490  
467 ..... 467  
490 aHisIleArgValProSerPheAlaAlaGlyArgValIleGlyLysGlyG 507  
467 ..... 467  
507 lYlYsThrValAsnGluLeuGlnAsnLeuSerSerAlaGluValVal 523  
467 ..... 467  
524 ProArgAspGlnThrProAspGluAsnAspGlnValValValLysIleTh 540  
468 ..... GACCAGACACCTGATGAGATGACCAAGTGGTTGTCAAAATAC 511  
540 rGlyHisPheTyrAlaCysGlnValAlaGlnArgLysIleGlnGluIleL 557  
512 TGGTCACCTTCTATGCTTCCAGGTTGCCAGAGAAAATTCAGGAAATTC 561  
557 euThrGlnValLysGlnHisGlnGlnLysAlaLeuGlnSerGlyPro 573  
562 TGACTCAGGTAAAGCAGCAGCAACAAGAGGCTCTGCAAAAGTGACCA 611  
574 ProGlnSerArgArgLys 579  
612 CCTCAGTCAAGACGGAAG 629

seq\_name: /cgn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq:PCT-US01-08631-12584

seq\_documentation\_block:  
; Sequence 12584, Application PC/TUS0108631  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-049  
; CURRENT APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom



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; SEQ ID NO 12584
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (3)..(1469)
; OTHER INFORMATION: 31% homologous to Herpesvirus papio NTR, accession number
; OTHER INFORMATION: AF200364, Smith-Waterman Score=247.
PCT-US01-08631-12584

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alignment_scores:
  Quality: 775.50      Length: 558
  Ratio: 3.783        Gaps: 3
  Percent Similarity: 36.738  Percent Identity: 34.588

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alignment\_block:

US-09-466-396A-176 x PCT-US01-08631-12584 ..

Align seg 1/1 to: PCT-US01-08631-12584 from: 1 to: 1998

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21 ILePheLysAlaLysIleProValSerGlyProPheLeuValLysTh 37
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3 ATCTGAAGACGCCAAGATCCCGTCTCGGACCCCTTCTCGTGAAGAT 52
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37 rGlyTyrAlaPheValAspCysProAspGluSerTrpAlaLeuLysAlaI 54
|||||
53 TGGCTACGCGTCTGCTGACTGCCACAGAGATCTGGCCCTCAAGGCCA 102
|||||
54 leGluAlaLeuSerGlyLysIleGluLeuHisGlyLysProIleGluVal 70
|||||
103 TTGAGGCGCTTCAGGTAAATAGAACTGCACGGGAACCATAGAAGTT 152
|||||
71 GluHisSerValProLysArgGlnArgIleArgLysLeuGlnIleArgAs 87
|||||
153 GACCACTCGTCCCAAAAGGCAC..... 176
|||||
87 nIleProHisLeuGlnTrpGluValLeuAspSerLeuLeuValcInt 104
|||||
176 ..... 176
104 yrGlyValValGluSerCysGluGlnValAsnThrAspSerGluThrAla 120
|||||
176 ..... 176
121 ValValAsnValThrTyrSerSerLysAspGlnAlaArgGlnAlaLeuAs 137
|||||
176 ..... 176
137 pLysLeuAsnGlyPheGlnLeuGluAsnPheThrLeuLysValAlaTyrI 154
|||||
176 ..... 176
154 leProaspGluMetAlaAlaGlnGlnAsnProLeuGlnGlnProArgGly 170
|||||
176 ..... 176
171 ArgArgGlyLeuGlyGlnArgGlySerSerArgGlnGlySerProGlyse 187
|||||
176 ..... 176
187 rValSerLysGlnLysProCysAspLeuProLeuArgLeuValProT 204
|||||
176 ..... 176
204 hrGlnPheValGlyAlaIleIleGlyLysGluGlyAlaThrIleArgAsn 220
|||||
176 ..... 176
221 IleThrLysGlnThrGlnSerLysIleAspValHisArgLysGluAsnAl 237
|||||
177 .....CACGGTAAAGAAAATGC 193

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237 aGlyAlaAlaGluLysSerIleThrIleLeuSerThrProGluGlyThrS 254
|||||
194 AGGGCTGCTGAGAAGTCGATTACTATCCTCTACTCCTGAAGGCACCT 243
|||||
254 erAlaAlaCysLysSerIleLeuGluIleMetHisLysGluAlaGlnAsp 270
|||||
244 CTCGGCTTCTAAGTCTATTCTGGAGATTATCGCTAAGGAACTCAAGAT 293
|||||
271 IleLysPheThrGluGluIleProLeuLysIleLeuAlaHisAsnAspPh 287
|||||
294 GTAAATTCACAGAAGAT..... 311
|||||
287 eValGlyArgLeuIleGlyLysGluGlyArgAsnLeuLysLysIleGluG 304
|||||
311 ..... 311
304 lNAspThrAspThrLysIleThrIleSerProLeuGlnGluLeuThrLeu 320
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311 ..... 311
321 TyrAsnProGluArgThrIleThrValLysGlyAsnValGluThrCysAl 337
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311 ..... 311
337 aLysAlaGluGluIleMetLysLysIleArgGluSerTyrGluAsnA 354
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311 ..... 311
354 spIleAlaSerMetAsnLeuGlnAlaHisLeuIleProGlyLeuAsnLeu 370
|||||
311 ..... 311
371 AsnAlaLeuGlyLeuPheProThrSerGlyMetProProThrSe 387
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311 ..... 311
387 rGlyProProSerAlaMetThrProProTyrProGlnPheGluGlnSerG 404
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311 ..... 311
404 luThrGluThrValHisGlnPheIleProAlaLeuSerValGlyAlaIle 420
|||||
312 .....GTTCAATCTGTTTATCCCGCTCTATCAGTCAGACGCCCTC 350
|||||
421 IleGlyLysGlnGlyGlnHisIleLysGlnLeuSerArgPheAlaGlyAl 437
|||||
351 ATCAGCAAGCAGGCCACACATCAACAGCAGCTTCTCGCTTTCCTGGAGC 400
|||||
437 aSerIleLysIleAlaProAlaGluAlaProAspAlaLysValArgMetV 454
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401 TTCAAGTAAGATTGCTCCAGTGGGAAGCACCAGATGCTAAGGTAGGATGG 450
|||||
454 alIleIleThrGlyProProGluAlaGlnPheLysAlaGlnGlyArgIle 470
|||||
451 TGATGATCGCTGCT..... 464
|||||
471 TyrGlyLysIleLysGluGluAsnPheValSerProLysGluGluValLy 487
|||||
464 ..... 464
487 sLeuGluAlaHisIleArgValProSerPheAlaAlaGlyArgValIleG 504
|||||
464 ..... 464
504 lLysGlyGlyLysThrValAsnGluLeuGlnAsnLeuSerSerAlaGlu 520
|||||
464 ..... 464
521 ValValValProArgAspGlnThrProAspGluAsnAspGlnValValVa 537
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465 ...GTTGCTCCCTTGTGACCACACACCTGATGAGAAATGACCAAGTGGTGT 511

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537 llystlethrGlyHisPheThrAlaCysGlnValAlaGlnArgLysIleG 554  
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512 CAAATAACTGCTCACTCTATGCTTGCAGGTGCCAGAGAAAATTC 561  
|||||  
554 InGluIleuThrGlnValLysGlnHisGlnGlnGlnLysAlaLeuGln 570  
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562 AGGAATTTCTGACTCAGGTAAAGCAGCAGCAACACAGAGGCTCTGCA 611  
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seq\_name: /cgn2\_6/ptodata/2/pna/PCT\_NEW\_COMB.seq: PCT-US01-08631-21953

seq\_documentation\_block:  
; Sequence 21953, Application PC/TUS0108631  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-049  
; CURRENT APPLICATION NUMBER: PCT/US01/08631  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 21953  
; LENGTH: 456  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIMILAR  
; LOCATION: (4)..(333)  
; OTHER INFORMATION: 98% homologous to Mus musculus igf2 mRNA-binding protein  
; OTHER INFORMATION: 3, accession number AB046173, Smith-Waterman Score=541.  
PCT-US01-08631-21953

alignment\_scores:  
Quality: 537.00 Length: 118  
Ratio: 4.752 Gaps: 1  
Percent Similarity: 95.763 Percent Identity: 94.068

alignment\_block:  
US-09-466-396A-176 x PCT-US01-08631-21953 ..

Align seg 1/1 to: PCT-US01-08631-21953 from: 1 to: 456

402 GlnSerGluThrGluThrValHisGlnPheIleProAlaLeuSerValG1 418  
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4 CAATCAGAAACGAGACTGTTTCATCTGTTATCCAGCTCTATCAGTCGG 53  
|||||  
418 ValAlleIleGlyLysGlnGlyGlnHisThrLysGlnLeuSerArgPheA 435  
|||||  
54 TCCCATCATCGCAAGCAGGCCACATCAAGCAGCTTCTCCGCTTG 103  
|||||  
435 laGlyAlaSerIleLysIleAlaProAlaGluAlaProAspAlaLysVal 451  
|||||  
104 CTGGAGCTTCATTAAGATTGCTCCAGCGGAGCACCAGATGCTAAAGTG 153  
|||||  
452 ArgMetValIleIleThrGlyProProGluAlaGlnPheLysAlaGlnG1 468  
|||||  
154 AGGATGGTATTATACATCGACACAGGCTCAGTTCAAGGCTCAGGG 203  
|||||  
468 yArgIleThrGlyLysIleLysGluGluAsnPheValSerProLysGluG 485  
|||||  
204 AGCAATTTATGGAATAATTAAGAGAAACACTTTGTTAGTCTCTAAGAG 253  
|||||  
485 luValLysLeuGluAlaHisIleArgValProSerPheAlaAlaGlyArg 501  
|||||  
254 AGGTGAACCTGAAGCTCATATCAGAGTGCCATCTTTGCTGCTGGCAGA 303  
|||||

502 ValIleGlyLysGlyLysThrValAsnGlu.LeuGlnAsnLeuSerS 518  
|||||  
304 GTTATTGAAAAAGGAGCAAAACGCAAGTACTTCAGCAAAACCTGTGCA 353  
|||||  
518 er 518  
||  
354 GT 355

seq\_name: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq: US-60-253-652-10626

seq\_documentation\_block:  
; Sequence 10626, Application US/60253652  
; GENERAL INFORMATION:  
; APPLICANT: Glenn, Matthew  
; TITLE OF INVENTION: Compositions isolated from bovine  
; TITLE OF INVENTION: tissues and methods for their use.  
; FILE REFERENCE: 1055P2  
; CURRENT APPLICATION NUMBER: US/60/253,652  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 29954  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10626  
; LENGTH: 516  
; TYPE: DNA  
; ORGANISM: Bovine  
; US-60-253-652-10626

alignment\_scores:  
Quality: 422.50 Length: 147  
Ratio: 3.912 Gaps: 1  
Percent Similarity: 73.469 Percent Identity: 61.224

alignment\_block:  
US-09-466-396A-176 x US-60-253-652-10626 ..

Align seg 1/1 to: US-60-253-652-10626 from: 1 to: 516

426 GlnHisIleLysGlnLeuSerArgPheAlaGlyAlaSerIleLysIleAl 442  
|||||  
44 CAGCACTGTCGCCATCTTCTCGGGCTCCTGCCATCTCTTGGGGCGGAG 93  
|||||  
442 aProAlaGluAlaProAspAlaLysValArgMetValIleIleThrGlyP 459  
|||||  
94 GCCACCATCAGGCGCAGATGTATCCTGCAGAGGCTGTCCCGTGGGCG 143  
|||||  
459 roProGlu..... 461  
||  
144 CAGGCCATTAACTTTACCCACTGTAAATCAGTCAACCTTTGGCCTTTCC 193  
|||||  
462 .....AlaGlnPheLysAlaGlnGlyAr 469  
|||||  
194 TACCTGAATGACACTGATAGGCTATGTTCTCATCTGTAGGCTCAGGGA 243  
|||||  
469 gIleThrGlyLysIleLysGluGluAsnPheValSerProLysGluGluV 486  
|||||  
244 AATTATGAAAAATTAAGAGAAATTTTGTAGTCTTAAGAGAGAG 293  
|||||  
486 alLysLeuGluAlaHisIleArgValProSerPheAlaAlaGlyArgVal 502  
|||||  
294 TGAACCTTGAAGCTCACATCAGAGTCCGCTCTTTGCTGGCAGAGTT 343  
|||||  
503 IleGlyLysGlyLysThrValAsnGluLeuGlnAsnLeuSerSerAl 519  
|||||  
344 ATTGAAAAGGAGGCAAAACGGTGAATCAGCTCCAGATTTGTCAAGTGC 393  
|||||  
519 aGluValValValProArgAspGlnThrProAspGluAsnAspGlnValV 536  
|||||  
394 AGAAGTTGTTTCCCGCTGACACACTCCTGATGAGAATGACCAAGTGG 443  
|||||  
536 alValLysIleThrGlyHisPheThrAlaCysGlnValAla 549  
|||||

```
|||||
444 TCGTCAGATAACTGGTCACCTTCTATCTGCTGCCAGGCAAGT 484
seq_name: /cgn2_6/ptodata/2/pna/us60_NEW_COMB.seq:US-60-253-652-21454
seq_documentation_block:
; Sequence 21454, Application US/60253652
; GENERAL INFORMATION:
; APPLICANT: Glenn, Matthew
; APPLICANT: Grigor, Murray R
; TITLE OF INVENTION: Compositions isolated from bovine
; TITLE OF INVENTION: tissues and methods for their use.
; FILE REFERENCE: 1055p2
; CURRENT APPLICATION NUMBER: US/60/253,652
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 29954
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21454
; LENGTH: 273
; TYPE: DNA
; ORGANISM: Bovine
US-60-253-652-21454

alignment_scores:
  Quality: 401.00      Length: 91
  Ratio: 4.557        Gaps: 0
  Percent Similarity: 96.703  Percent Identity: 86.813
alignment_block:
US-09-466-396A-176 x US-60-253-652-21454  ..
Align seg 1/1 to: US-60-253-652-21454 from: 1 to: 273
429 LysGlnLeuSerArgPheAlaGlyAlaSerIleLysIleAlaProAlaG1 445
1 AAGCAGCTCTCCGGTTCGCCAGGCGCTCCATCAAGATTGCTCTCTCGA 50
445 uAlaProAspAlaLysValArgMetValIleIleThrGlyProProGluA 462
51 AACTCCAGACTCCAAGTTCGTATGTTGTCATCATCTACATGGAGCCGCCAAG 100
462 laGlnPheLysAlaGlnGlyArgIleThrGlyLysIleLysGluGluAsn 478
101 CCCAGTTCACAGGCTCAGGGAAGATTTATGGAAACTCAAGGAGGAGAAC 150
479 PheValSerProLysGluGluValLysLeuGluAlaHisIleArgValPr 495
151 TTCCTTGGTCCCAAGGAGAGAGTAAAGCTGGAGACCATTATCCGGGTGCC 200
495 oSerPheAlaAlaGlyArgValIleGlyLysGlyGlyLysThrValAsnG 512
201 AGCGTCAGCAGCGCGCGGCTCATTTGGCAAAAGSTGGCAAGACGGTGAATG 250
512 luLeuGlnAsnLeuSerSerAla 519
251 AGCTGCAAAATTTGACAGCAGCT 273
seq_name: /cgn2_6/ptodata/2/pna/us60_NEW_COMB.seq:US-60-278-232-4474
seq_documentation_block:
; Sequence 4474, Application US/60278232
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence databases, and Single Nucleotide
; FILE REFERENCE: GX-0011 P
; CURRENT APPLICATION NUMBER: US/60/278,232
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 12,557
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```
; SOFTWARE: PERL Program
; SEQ ID NO 4474
; LENGTH: 4628
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 234498.6
; NAME/KEY: unsure
; LOCATION: 2161
; OTHER INFORMATION: a, t, c, g, or other
US-60-278-232-4474

alignment_scores:
  Quality: 235.50      Length: 449
  Ratio: 1.056        Gaps: 18
  Percent Similarity: 49.666  Percent Identity: 22.272
alignment_block:
US-09-466-396A-176 x US-60-278-232-4474  ..
Align seg 1/1 to: US-60-278-232-4474 from: 1 to: 4628
161 GlnGlnAsnProLeuGln.....GlnProArgGlyArgArgGlyLe 174
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
280 CAAAAAGACCTTTAGAGATGGAGATCAACCAGATGCTAAGAAAGTTGC 329
174 uGlyGlnArgGlySerArgGlnGlySerProGlySerValSerLysG 191
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
330 TCCTCAAAATGACTCTTTTGGAACACAGTTACCA...CCGATGCATCAGC 376
191 InLysProCysAspLeuProLeuArgLeuLeuValProThrGlnPheVal 207
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
377 AGCAAGATCTGTAATGACACAGAAATACAAAGTTCAGATGGAATGCTT 426
208 GlyAlaIlelleGlyLysGluGlyAlaThrIleArgAsnIleThrLysG1 224
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
427 GGATTCTAATTTGGCAGAGGAGTCAACAGATCTCACGCATACACAGGA 476
224 nThrGlnSerLysIleAspValHisArgLysGluAsnAlaGlyAlaAlaG 241
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
477 ATCTGGATGCANAATACAGATA...GCTCCTGACAGTGGTGGCCTTCCAG 523
241 luLysSerIleThrIleLeuSerThrProGluGlyThrSerAlaAlaCys 257
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
524 AAGGTCTCTGTATGTTAACTGGACACCTGAATCTGTCCAGTCAGCAAAA 573
258 LysSerIleLeuGluIleMetHisLysGluAlaGlnAspIleLysPheTh 274
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
574 CGGTTACTGGACACAGATGTTTCAAAAAGGAAGACGAGCTCCTGGCTCCA 623
274 rGlu.....GluIleProLeuLysIleLeuAlaHisAsnA 286
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
624 TCATGGCGATGGACGGAAATGCAGTTTCAAGAAATCATGATTCAGCTA 673
286 snPheValGlyArgLeuIleGlyLysGluGlyArgAsnLeuLysLysIle 302
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
674 GCAAGCAGGAGTATAGTCATGGAAAAGGGCGAGAACTATTAAACAGCTT 723
303 GluGlnAspThrAspThrLysIleThrIleSerProLeuGlnGluLeuTh 319
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
724 CAGGAACGGGCTGGAGTTAAATGGTTATG.....ATTCAAGAC..... 762
319 rLeuTyrAsnProGluArgThr.....IleThrValLysG 331
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
763 .....GGGCCGACAGACACTGGTGTGACAAACCTCTTAGGATTACAG 805
331 lyAsnValGluThrCysAlaLysAlaGluGluIleMetLysLysIle 347
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
806 GAGACCCATATAAAGTTCAACACCAAGCAAGAAATGGTGTAGAGTTAATT 855
348 ArgGlu.....SerTyrGluAsnAspIleAlaSerMetAs 359
```



```

829 ..... ||| |||
380 erGlyMetProProThrSerGlyProProSerAlaMetThrProPro 396
|||
848 TGGGA.....
397 TyrProGlnPheGluGlnSerGluThrGluThrValHisGlnPheLePr 413
:||||: ||| :|||
853 .....GGAGGCAGTATAGAGGTATCTGTGCC 878
413 oAlaLeuSerValGlyAlaIleIleGlyLysGlnGlyGlnHisIleLysG 430
| :||||: ||| :||||: ||| :||||: ||| :||||: ||| :||||: |||
879 TAGGTTGCTGTGGGATTGTAATAGAGAAACGGGGAATGATCAAAA 928
430 InLeuSerArgPheAlaGlyAlaSerIleLysIleAlaProAlaGlu... 445
:||||: ||| :||||: ||| :||||: ||| :||||: ||| :||||: |||
929 AGATCCAGATGATGCTGGTGTGAGGATTCAGTTTAAACCATGATGGG 978
446 ...AlaProshAlaLysValArgMetValIleIleThrGlyProGln 461
:||||: ||| :||||: ||| :||||: ||| :||||: ||| :||||: |||
979 ATTAGTCCAGAA.....AGAGTGCCAGGTATGCGCCCTCCGGA 1019
461 u.....AlaG 463
1020 TCGGTGTACATGCAGCGCATATCATCAGCAGCTGATTCTTACAGCCC 1069
463 InPheLys.....AlaGlnGlyArgIleTyr 471
||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1070 AGAAGAGACGCGCTTGGAGGCTGGCAGCAGCCAGAGGA..... 1113
472 GlyLysIleLysGluGlnAsnPheValSerProLysGluGluValLysLe 488
:||||: ||| :||||: ||| :||||: ||| :||||: ||| :||||: |||
1114 GGTGCTGGCGTGGCGACTGGAGCTGGGAGCCCTGGTGGCGTCCAG.. 1161
488 uGluAlaHisIleArgValProSerPheAlaAlaGlyArgValIleGlyL 505
||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1162 .GAGATAACATACACGGTGTCCAGCCGATAAGTGGCGCTGTCATAGGCA 1210
505 ysGlyGlyLysThrValAsnGluLeuGlnAsnLeuSerSerAlaGluVal 521
||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1211 AAGGGGTGAGACATCAAAAGCATCAACAGCAGTCAGGGGGCGCAGTG 1260
522 ValValProArgAspGlnThrProAspGluAsnAspGlnVal...ValVa 537
:||||: ||| :||||: ||| :||||: ||| :||||: ||| :||||: |||
1261 GAGCTTCAGAGGAACCCCTCCCAACAGCAGCCCAACCTCGGAGATT 1310
537 LysIleThrGlyHisPheTyrAlaCysGlnValAlaGlnArgLysIleG 554
||| ||| :||||: ||| :||||: ||| :||||: ||| :||||: |||
1311 CACCATCAGGGGGTTCCTCCAGCAGATCGAGGTGGCGCAGGAGCTCATAG 1360
554 InGlu 555
:||||
1361 ATGAG 1365

```

seq\_name: /cgn2\_6/ptodata/2/pna/US60\_NEW\_COMB.seq:US-60-278-258-15023

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seq_documentation_block:
; Sequence 15023, Application US/60278258
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preethi
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
; TITLE OF INVENTION: Polymorphisms Identified Thereby
; FILE REFERENCE: GX-0010-1 P
; CURRENT APPLICATION NUMBER: US/60/278,258
; CURRENT FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 17730
; SOFTWARE: PERL Program
; SEQ ID NO 15023
; LENGTH: 4175

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```

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 333997.1
; NAME/KEY: unsure
; LOCATION: 112, 145, 147, 190, 227, 230, 246, 251, 265, 277, 307, 309, 311, 315,
; LOCATION: 318, 326, 333, 335, 346, 362, 368, 468-511
; OTHER INFORMATION: a, t, c, g, or other
US-60-278-258-15023

```

# alignment\_scores:

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Quality: 227.00 Length: 531
Ratio: 0.934 Gaps: 20
Percent Similarity: 45.763 Percent Identity: 22.411

alignment_block:
US-09-466-396A-176 x US-60-278-258-15023 ..
Align seg 1/1 to: US-60-278-258-15023 from: 1 to: 4175

155 ProAspGluMetAlaAlaGlnGlnAsnProLeuGlnGlnProArgGlyAr 171
||||| :||||: ||| :||||: ||| :||||: ||| :||||: |||
635 CCGGAC.....TCGCGAAAGGCCGCTGGAGCCCC..... 667

171 gaGgGlyLeuGlyGlnArgGlySerArgGlnGlySerProGlySerV 188
:||||: ||| :||||: ||| :||||: ||| :||||: ||| :||||: |||
668 .....CCTGAAGCCGCGCAGCACCAGAGGACCAATACGGCGGAAG 707

188 alSerLysGlnLysProCysAspLeuProLeuArgLeuLeuValProThr 204
:||||: ||| :||||: ||| :||||: ||| :||||: ||| :||||: |||
708 ACGGCCAGTATTTT.....CTAAAGGTCTCATACCTAGT 742

205 GlnPheValGlyAlaIleIleGlyLysGluGlyAlaThrIleArgAsnIl 221
:||||: ||| :||||: ||| :||||: ||| :||||: ||| :||||: |||
743 TATGCTGCTGGATCTAATAATGGAGGGAGGACAGACAATTTTCAGTT 792

221 eThrLysGlnThrGlnSerLysIleAspValHisArgLysGluAsnAla. 237
:||||: ||| :||||: ||| :||||: ||| :||||: ||| :||||: |||
793 GCAAAAGAAACTGGAGCCACCACCAAGCTCTAAGCTGCTTAAGTCCA 842

238 .....GlyAlaAlaGluLysSerIleThrIleLeuSerThr 249
:||||: ||| :||||: ||| :||||: ||| :||||: ||| :||||: |||
843 AAGATTTTACCAGGTACTACTGAGCGAGTGTGCTTGCATCCAGGGAAG 892

250 ProGluGlyThrSerAlaAlaCysLysSerIleLeuGluIleMetHisLy 266
:||||: ||| :||||: ||| :||||: ||| :||||: ||| :||||: |||
893 GTTGAAGCACTGAATGCAGTTCATGGATTTCATTCGAGAAAAAATTCGA 942

266 sGluAlaGlnAspIleLysPheThrGluGluIleProLeu..... 279
:||||: ||| :||||: ||| :||||: ||| :||||: ||| :||||: |||
943 AATGCCCAAAATGTGCCAAGACAGACACCAGTCAGCATTCACAAACCCC 992

279 ..... 279

993 AGACCACCGTTAATCCAGATCGCATCAACAAACATTTGCCATCTTCCCA 1042

279 ..... 279

1043 ACTACCACCAAGTCCTCTCCATCTGATCCCATGACCACTCCAGAGCTAA 1092

280 .....LysIleLeuAlaHisAsnAsnPheValGlyArgLeuIleGlyL 294
||||| :||||: ||| :||||: ||| :||||: ||| :||||: |||
1093 TCAGGTAAAGATTATAGTTCCCAACACAGCAGAGGTCTGTATATAGGA 1142

294 ysGluGlyArgAsnLeuLysIleGluGlnAspThrAspThrLysIle 310
||| ||| :||||: ||| :||||: ||| :||||: ||| :||||: |||
1143 AGGAGGTGCTACTGTCAAGGCTGTAATGGAGCAGTCAGGGGCTTGGGTG 1192

311 ThrIleSerProLeuGlnGluLeuThrLeuTyrAsnProGluArgThrIl 327
:||||: ||| :||||: ||| :||||: ||| :||||: ||| :||||: |||
1193 CAGCTTCCCAAGAACCTGAT...GGGATCAACTTGAAGAGAGGGTGT 1239

```

```
327 eThrValLysGlyAsnValGluThrCysAlaLysAlaGluGluIleM 344
      ::::::::::::::: ||| ||||| |||
1240 CACTGTGAGTGGAGAACCTGAACAAACCGAAAGCTGTGAATATCA 1289
      ||| ||| ::::::::::::::: Ser 350
344 eLysLysLysIleArgGlu.....
      ::::::::::::::: |||
1290 TCCAGAAAGATACAAGAGGATCCACAAAGTGGCAGCTGTCTCAATATCAGT 1339
      ||| ||| :::::::::::::::
351 TyrGluAsn.....AspIleAlaSerMetAsn..... 359
      ||| ||| ::::::::::::::: |||
1340 TATGCCAATGTACAGGTCACCTGTCGCAATTCATCCACCGGATCTCC 1389
      ||| ||| :::::::::::::::
360 .....LeuGlnAlaHisL 364
      ||| ||| ::::::::::::::: |||
1390 TTATGCAAAACACTGCTGAAGTCTTACCAACTGCTGCAGCAGCTGCAGGC 1439
      ||| ||| :::::::::::::::
364 euIleProGlyLeuAsnLeuAsnAlaLeuGlyLeuPheProThr... 379
      ||| ||| ||||| ::::::::::::::: |||
1440 TATTAGGACATGTAACCTTGTCTGCGTGTGCAGCCTTTCCACAGCTTTA 1489
      ||| ||| ::::::::::::::: |||
380 SerGlyMetProProThrSerGlyProProSerAlaMetThrProPr 396
      ||| ||| ::::::::::::::: |||
1490 TCTGGCTC.....ACAGCAATGACCTGTGGCGCATCACCC..... 1525
      ||| ||| ::::::::::::::: |||
396 oTyrProGlnPheGluGlnSerGluThrGluThrValHisGlnPheIleP 413
      ||| ||| ::::::::::::::: |||
1526 .....TCTGCACTTAATACATTA..... 1543
      ||| ||| ::::::::::::::: |||
413 roAlaLeuSerValGlyAlaIleIleGlyLysGlnGlyClnHisIleLys 429
      ||| ||| ||||| ::::::::::::::: |||
1544 .....GCCAGCTATGGTATATATCTCAACACTTTTAGGTTTAGGTCCTCAGT 1588
      ||| ||| ::::::::::::::: |||
430 GlnLeuSerArgPheAlaGlyAlaSerIleLysIleAlaProAlaGluAl 446
      ||| ||| ::::::::::::::: |||
1589 CAAGCAGCAGCA...ACAGGGCTTGGCTGCAGCAGCTGCAGTGCCCA 1635
      ||| ||| ::::::::::::::: |||
446 aProAspAlaLysValArgMetValIleIleThrGlyProProGluAlaG 463
      ||| ||| ::::::::::::::: |||
1636 CCCAGCAGCAGCAGCAGCAATTTATTTGGCCACCTATGCCAGTGAAGCT 1685
      ||| ||| ::::::::::::::: |||
463 InPheLys..... 465
      ||| ||| ::::::::::::::: |||
1686 CAGCCAGTGGCAGCAGCAGCTGTGTGACGGGGGACATTTGCATTAGGT 1735
      ||| ||| ::::::::::::::: |||
465 ..... 465
      ||| ||| ::::::::::::::: |||
1736 AGCCTGGCTGCTGCTACTGCTGCACCAATGGATATTTTGGAGCTGCTC 1785
      ||| ||| ::::::::::::::: |||
466 .....AlaGlnGlyArgIleTyrGlyLysIleLysGluGluAsnPheV 480
      ||| ||| ::::::::::::::: |||
1786 TCCCTCCTAGTGCCTGCTGCTGCTAGGA.....ACAGAAAAGTCCACAG 1829
      ||| ||| ::::::::::::::: |||
480 aLysProLysGluGluValLysLeuGluAlaHisIleArgValProSer 496
      ||| ||| ::::::::::::::: |||
1830 ATGGATCCAGGATAGTGTGAA.....ATAGCAGTGCAGAA 1867
      ||| ||| ::::::::::::::: |||
497 PheAlaAlaGlyArgValIleGlyLysGlyLysThrValAsnGluLe 513
      ||| ||| ::::::::::::::: |||
1868 NACTTAGTGGTGCATCTTGGCAAGAGGAGGAAACATTTAGTGAATA 1917
      ||| ||| ::::::::::::::: |||
513 uGlnAsnLeuSerSerAlaGluValValProArg.....AspGlnT 528
      ||| ||| ::::::::::::::: |||
1918 CCAGGAGTGTGCTGTAAGGATACAGATCTCCAAAAAGAGAAATTCG 1967
      ||| ||| ::::::::::::::: |||
528 hrProAspGluAsnAspGlnValValLysIleThrGlyHisPheTyr 544
      ||| ||| ::::::::::::::: |||
1968 TACTTGGCAGCAGGAAATCGAAGGTAAACC...ATTACTGGAAACACCACT 2014
      ||| ||| ::::::::::::::: |||
545 AlaCysGlnValAlaClnArgLysIleGlnGluIleLeuThrGlnVal 561
      ||| ||| ||||| ||| ::::::::::::::: |||
2015 GCACACAGGCTGCTCAATATTTAATTACACAAGGATCACA..... 2056
      ||| ||| ::::::::::::::: |||
```

```
561 scInHisGlnGlnLysAlaLeuGlnSerGlyProProGln 575
      ::::::::::::::: |||
2057 .....TATGACGAAGGAGTTGGGCTGCCAATCCTCAG 2089
      ||| ||| ::::::::::::::: |||
seq_name: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq:US-60-278-232-11258

seq_documentation_block:
; Sequence 11258, Application US/60278232
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide
; FILE REFERENCE: GX-0011 P
; CURRENT APPLICATION NUMBER: US/60/278,232
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 12,557
; SOFTWARE: PERL Program
; SEQ ID NO 11258
; LENGTH: 3316
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No: 902614.14
; NAME/KEY: unsure
; LOCATION: 3256
; OTHER INFORMATION: a, t, c, g, or other
US-60-278-232-11258
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alignment_scores:
Quality: 217.50 Length: 534
Ratio: 0.853 Gaps: 26
Percent Similarity: 47.753 Percent Identity: 23.408

alignment_block:
US-09-466-396a-176 x US-60-278-232-11258 ..

Align seg 1/1 to: US-60-278-232-11258 from: 1 to: 3316

104 TyrGlyValValGluSerCysGluGln.ValAsnThrAspSerGluThrA 120
      ::||| ||| ||| ::||| |||
457 TACTACTTTATTCTAGATTGACGCCAAATTTGGAGCGATGCTGCCAGA 506
      ||| ||| ::||| |||
120 laValValAsnValThr.....TyrSerSerLysAspGlnAlaArgGln 134
      ::||| ||| ||| ::||| |||
507 CAGTGAATAACAGCAGCTCTGATTGTTGTTGGGGGCCCAAGAGACAG 556
      ||| ||| ||| |||
135 AlaLeuAspLysLeuAsnGlyPheGlnLeuGluAsnPheThrLeuLysVa 151
      ||| ||| ||| |||
557 TTGGAGAT.....GGAGATCAACCGGAG.....AGCAAGAAGCT 591
      ||| ||| ::||| |||
151 AlaTyrIleProAspGluMetAlaAlaGlnGlnAsnProLeuGlnGlnP 168
      ||| ||| ::||| |||
592 GCCTTCCCAGGGAGACTCAATCAGTTCTCAACTTGGACCCATCCATCCTC 641
      ||| ||| ::||| |||
168 roArgGlyArgArgGlyLeuGlnArgGlySerSerArgGlnGlySer 184
      || ||| |||
642 CC.....CCAAGGACTTCAATGACAGAA..... 664
      ||| |||
185 ProGlySerValSerLysGlnLysProCysAspLeuProLeuArgLeuLe 201
      ||| |||
665 .....GAGTACAG 672
      ||| |||
201 uValProThrGlnPheValGlyAlaIleGlyLysGluGlyAlaThrI 218
      ||| ||| ::||| |||
673 GGTCCACAGCGCATGGTGGGCTGATCATTTGGCAGAGGAGTGAACAA 722
      ||| ||| ::||| |||
218 leArgAsnIleThrLysGlnThrGlnSerLysIleAspValHisArgLys 234
      ||| ||| ::||| |||
```

```
723 TTAACAAATCCAAAGGATTACGGTGTCAAGTACAGATT...TCTCCA 769
235 GluAsnAlaGlyAlaAlaGluLysSerIleThrIleLeuSerThrProG1 251
770 GACAGGGGTGGCTACCCAGGCGCATGTGTCTTTCACAGAGGAGCCCA 819
251 uGlyThrSerAlaAlaCysLysSerIleLeuGluIleMet..... 264
820 ATCTGTCCAGAAAGCAAGATGATGCTGGATGACATTTGTCTCTCGGGGTC 869
265 .....HisLysGluAla.....GlnAsp 270
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; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)A
; CURRENT APPLICATION NUMBER: US/60/312,544
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 10730
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209 alleIleGlyLysGluGlyAlaThrIleArgAsnIleThrLysGlnThr 226
543 TATCATTTGGCGCAAGGGAGTTTATCAAGAGATGTGCGAGGAGACTA 592
226 lnSerLysIleAspValHisArgLysGluAsnAlaGlyAlaAlaGluLys 242
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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 29, 2001, 06:22:32 ; Search time 4669.91 Seconds  
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13229.772 Million cell updates/sec

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	4165	99.6	4181	US-09-543-615A-175	Sequence 175, App
3	4165	99.6	4181	US-09-606-421A-175	Sequence 175, App
4	4165	99.6	4181	US-09-630-940A-175	Sequence 175, App
5	4165	99.6	4181	US-09-630-940B-175	Sequence 175, App
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7	4165	99.6	4181	US-09-662-786-175	Sequence 175, App
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9	4165	99.6	4181	US-09-735-705-175	Sequence 175, App
10	4165	99.6	4181	US-09-850-716-175	Sequence 175, App
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14	3987	95.4	4430	US-60-172-360-28769	Sequence 28769, A
15	1736.8	41.5	1740	US-09-543-615A-347	Sequence 347, App
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29	820.4	19.6	2512	US-09-617-182-2240	Sequence 2240, Ap
30	744	17.8	843	US-09-399-932-4493	Sequence 4493, Ap
31	720	17.2	834	US-09-652-123-8442	Sequence 8442, Ap
32	710.4	17.0	3374	PCT-US01-01307-113	Sequence 113, App
33	710.4	17.0	3412	US-09-061-709-6	Sequence 6, Appli
34	710.4	17.0	3412	US-09-270-437-6	Sequence 329, App
35	699.4	16.7	3694	PCT-US01-01341-3295	Sequence 3295, A
36	699.4	16.7	3650	US-60-172-360-27652	Sequence 27652, A
37	695.6	16.6	3283	US-09-061-709-8	Sequence 8, Appli
38	695.6	16.6	3283	US-09-270-437-8	Sequence 8, Appli
39	695.6	16.6	3896	US-09-644-869-8906	Sequence 8906, Ap
40	695.6	16.6	3896	US-09-699-998-9743	Sequence 9743, Ap
41	695.6	16.6	3896	US-09-721-589-6556	Sequence 6556, Ap
42	672.6	16.1	1946	US-09-061-709-7	Sequence 7, Appli
43	672.6	16.1	1946	US-09-270-437-7	Sequence 7, Appli
44	580.6	13.9	1708	US-09-061-709-5	Sequence 5, Appli
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; Sequence 175, Application US/09630940B  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqu  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.455C10  
; CURRENT APPLICATION NUMBER: US/09/630,940B  
; CURRENT FILING DATE: 2000-08-02  
; NUMBER OF SEQ ID NOS: 367



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; APPLICANT: Wang, Tongtong  
; APPLICANT: Fan, Liqun  
; APPLICANT: Kalos, Michael D.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Hosken, Nancy  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Li, Samuel X.  
; APPLICANT: Wang, Aijun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: McNeill, Patricia D.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.455C13  
; CURRENT APPLICATION NUMBER: US/09/685,696  
; CURRENT FILING DATE: 2000-10-09  
; NUMBER OF SEQ ID NOS: 381  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 175  
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; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:

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Query Match 99.6%; Score 4165; DB 27; Length 4181;  
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; Sequence 175, Application US/09735705
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 175
; LENGTH: 4181
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: unsure

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RESULT 9  
US-09-735-705-175

03 03 703 175 ; Sequence 175, Application US/09735705

GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Fan, Lique

APPLICANT: Kalos, Michael D.

: APPLICANT: Banpur, Chaitanya S.

APPLICANT: Hosken, Nancy

APPLICANT: Fanger, Gary R

APPLICANT: I.i. Samuel X

APPLICANT: Wang Aijun

APPLICANT: WANG, ALJUN  
APPLICANT: SKEIKY YASIR A W

APPLICANT: SKELTY, IASII A.W.  
 : HENDERSON Robert A

APPLICANT: McNeill Patricia D  
APPLICANT: Henderson, Robert A

APPLICANT: McNeill, Patricia  
 ADDRESS: Fargo, North Dakota

APPLICANT: Fanger, Neil  
TITLE OF INVENTION: COMPOSTIONS AND METHODS FOR THE PURIFICATION OF WATER

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR

; TITLE OF INVENTION: AND DIAGN

; FILE REFERENCE: 210121.455C14

; CURRENT APPLICATION NUMBER: US/09/735,705

; CURRENT FILING DATE: 2000-12-12

; NUMBER OF SEQ ID NOS: 419

; SOFTWARE: FastSEQ for Windows Version 3.

; SEQ ID NO 175

; LENGTH: 4181

; TYPE: DNA

; ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: unsure









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Qy 4081 ataagttncccccataagcagcttctcatatttccaganaacttgcacgagataaaatttttc 4140  
Db 4081 ataagttncccccataagcagcttctcatatttccaganaacttgcacgagataaaatttttc 4140









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Db 3891 acataggtgctgcattt-atatctgctggttttaattctgtcatattttcaactcttagcct 3949
QY 3957 tttagtatgcnnaatcanaattttacttttaagcattttgtaatttgagtagtctggt 4016
Db 3950 tttagtatgcnnaatcnaattttacttttaagcattttgtaatttgagtagtctggt 4009
QY 4017 actagctaagaataattcnataattgattttgttactcnccaaanattggttcattctcc 4076
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QY 4077 atgnataatgttcccccaatgcagcttcattttccaganaaccttgacgcagagataaaatt 4136
Db 4070 atgataatgttcccccaatgcagcttcattttccagataaccttgacgcagagataaaatt 4129
QY 4137 ttctcattttagggtcc 4153
Db 4130 ttctcattttagggtgc 4146
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## RESULT 14

US-60-172-360-28769

; Sequence 28769, Application US/60172360

; GENERAL INFORMATION:

; APPLICANT: Morris, MacDonald

; APPLICANT: Lal, Preeti

; APPLICANT: Diep, Dinh

; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using

; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymorph

; FILE REFERENCE: GX-0007 P

; CURRENT APPLICATION NUMBER: US/60/172, 360

; CURRENT FILING DATE: 1999-12-16

; NUMBER OF SEQ ID NOS: 29838

; SOFTWARE: PERL Program

; SEQ ID NO 28769

; LENGTH: 4430

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; OTHER INFORMATION: Incyte ID No: 236315.6

; FEATURE:

; NAME/KEY: unsure

; LOCATION: 2204, 2212, 2216, 2222

; OTHER INFORMATION: a, t, c, g, or other

US-60-172-360-28769

Query Match 95.4%; Score 3987; DB 49; Length 4430;

Best Local Similarity 98.4%; Pred. No. 0;

Matches 4090; Conservative 0; Mismatches 50; Indels 15; Gaps 7;

QY 1 ggtgagtcggttggttagtacta-ggctttttctttctttctttcttttaaacacatc 59

Db 1 ggtgagtcggttggttgtagctacggctttttctttctttctttcttttaaacacatc 60

QY 60 tagacaagaaaaaacaagctcgatctgatttttcaactctctgtttctgttggtt 119

Db 61 tagacaagaaaaaacaagctcgatctgatttttcaactctctgtttctgttggtt 120

QY 120 ctactctgtttgttattttaagcgcagagagagaggggaacaaaccagctggatcc 179

Db 121 ctactctgtttgttattttaagcgcagagagaggggaacaaaccagctggatcc 180

QY 180 atccatcacccgtgggttggttttaattttttctgttttttttttttttttaaacac 239

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QY 240 caactctcaaatgaacaaactgtatatcggaacctcaagcagagacgcgcctcctcgg 299

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QY 539 ctggatagtttactagtcagtagtgagtggtggagagctgtgagcaagtgaacactgac 598
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QY 1859 gtcaaatcaactggtcactctctatgcttgcagggttcccagagaaaaattcaggaaatt 1918  
DB 1861 gtcaaatcaactggtcactctctatgcttgcagggttcccagagaaaaattcaggaaatt 1920  
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DB 1921 ctgactcaggtaagcagcagcccaacaacagaggctctgcaaatgaccacctcagtc 1980  
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DB 2101 acctagccagttgttctgaggaccaggcaacttttgaactcctctctctgtgagaatgt 2160  
QY 2159 atactttatgctctctgaaatgatgaccccttatccagaatccaaacaaacaaaca 2218  
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QY 2279 cacagtaacagatatcttaattctcttaattatcccccataatgccagaattggct 2338  
DB 2281 cacagtaacagatatcttaattctcttaattatcccccataatgccagaattggct 2340  
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## RESULT 15

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US-09-542-615A-347
; Sequence 347, Application US/09542615A
; GENERAL INFORMATION:
; APPLICANT: Wang, TongLong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542,615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 347
; LENGTH: 1740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-542-615A-347
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Query Match 41.5%; Score 1736.8; DB 21; Length 1740;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1738; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 251 atgaacaaactgtatctcgaaacccctcagcgagaacgcgccttcgacactagaagt 310
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4	710.4	17.0	2010	1	PCT-US01-08631-6785	Sequence 6785, Ap
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6	409.6	9.8	583	5	US-09-510-376A-100	Sequence 100, Appl
7	324.6	7.8	456	1	PCT-US01-08631-21953	Sequence 21953, A
8	237.2	5.7	516	6	US-60-253-652-10626	Sequence 10626, A
9	231.4	5.5	321	4	US-08-798-0748-12440	Sequence 12440, A
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12	225.2	5.4	315	1	PCT-US01-08631-21951	Sequence 21951, A
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14	173.2	4.1	383	6	US-60-253-652-6909	Sequence 6909, Ap
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RESULT 2
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; Sequence 21954, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc

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: APPLICANT: Hyseq, Inc
: TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
: FILE REFERENCE: 21272-049
: CURRENT APPLICATION NUMBER: PCT/US01/08631
: CURRENT FILING DATE: 2001-03-30
: PRIORITY APPLICATION NUMBER: 09/540,217
: PRIOR FILING DATE: 2000-03-31
: PRIOR APPLICATION NUMBER: 09/649,167
: PRIOR FILING DATE: 2000-08-23
: NUMBER OF SEQ ID NOS: 60736
: SOFTWARE: Custom
: SEQ ID NO 21954
: LENGTH: 4264
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Query Match 92.5%; Score 3865.6; DB 1; Length 4264;  
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; LOCATION: (1774)..(2013)
; OTHER INFORMATION: 55% homologous to Homo sapiens IGF-II mRNA-binding protein
; OTHER INFORMATION: 3, accession number AF117108, Smith-Waterman Score=204.
PCT-US01-08631-21954

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Db 4107 ttgtattttggagttactgtgactagtaagaataattcnaataattgagtttttactc 4166  
Qy 4056 nccaaanaattgggttacttctcagtaaatgtncnccccacagcttcattttccagan 4115  
Db 4167 accataatggtatcattctcagtaataatgtgcccaaatgagcttcattttccagan 4226  
Qy 4116 acctgacgcaggaataaatttttccatcttaggtcc 4153  
Db 4227 acctgacgcaggaataaatttttccatcttaggtgc 4264

RESULT 3  
PCT-US01-08631-12583  
; Sequence 12583, Application PC/TUS0108631  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-049  
; CURRENT APPLICATION NUMBER: PCT/US01/08631  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217

;; PRIOR FILING DATE: 2000-03-31  
;; PRIOR APPLICATION NUMBER: 09/649,167  
;; PRIOR FILING DATE: 2000-08-23  
;; NUMBER OF SEQ ID NOS: 60736  
;; SOFTWARE: Custom  
;; SEQ ID NO 12583  
;; LENGTH: 1985  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: SIMILAR  
;; LOCATION: (164)..(3)  
;; OTHER INFORMATION: 79% homologous to Homo sapiens Human secreted protein  
;; OTHER INFORMATION: HLYE538, SEQ ID NO:220,accession number Y86305,Smith-Waterman Soc  
;; OTHER INFORMATION: -211.  
PCT-US01-08631-12583

Query Match 43.98; Score 1837; DB 1; Length 1985;  
Best Local Similarity 96.4%; Pred. No. 0;  
Matches 1915; Conservative 1; Mismatches 57; Indels 14; Gaps 3;  
Qy 251 atgaacaaactgtatatcggaacactcagcgagacgcgcgccttcggaactagaaagt 310  
Db 1 atgaacaaacgctatatcagaaacactcagcgagacgcgcgccttcggaactagaaagt 60  
Qy 311 atcttcaggagcgcgaagatccccggtgtcgggaccccttcctgtggaagactggctacgcg 370  
Db 61 atcttgaaggagcgcgaagatccccggtgtcgggaccccttcctgtggaagactggctacgcg 120  
Qy 371 ttctggactccggagcagagactgggcccctcaaggccactcgaggcgtttcagggtaaa 430  
Db 121 ttctggactcccgacagagatctggccctcaaggccactcgaggcgtttcagggtaaa 180  
Qy 431 atgaactgcacgggaaacccatagaagttagcactcggtcccaaaaaaggcaagatt 490  
Db 181 atgaactgcacgggaaacccatagaagttagcactcggtcccaaaaaaggcaagatt 240  
Qy 491 cggaacttcagatcacgaatatccccctcatttacagtgggagggtcggtgagtagttta 550  
Db 241 cggaacttcagatcacgaatatccccctcatttacagtgggagggtcggtgagtagttga 300  
Qy 551 ctactcagatgagtggtgagagctgagcaagtgaacactgactcgggaactgca 610  
Db 301 ctactcagatgagtggtgagagctgagcaagtgaacactgactcgggaactgca 360  
Qy 611 gttgtaaatgtaacctattccagtaaggaccacaa-----gctagacaaagcactag 659  
Db 361 gttgtaaatgtaacctattccagtaaggaccacaaagctagacaaagcctagacaaagcactag 420  
Qy 660 acaactgaaatggaatttcagtagagaatttcacctgaaagtgcctatatccctgatg 719  
Db 421 acaactgaaatggaatttcagtagagaatttcacctgaaagtgcctatatccctgatg 480  
Qy 720 aaatggccgcacgaacaaaccccttcagcagcccgaggtcgccggggcttgggcaga 779  
Db 481 aaatggccgcacgaacaaaccccttcagcagcccgaggtcgccggggcttgggcaga 540  
Qy 780 ggggctcctcaaggcaggggtctccaggatccgtatccaagcagaacacacattgatttcg 839  
Db 541 ggggctcctcaaggcaggggtctccaggatccgtatccaagcagaacacacattgatttcg 600  
Qy 840 ctctgcctctgctggttcccaacccaaatttgttgagccatcaataggaagaagggtgcca 899  
Db 601 ctctgtgctgctggttcccaacccaaatttgttgagccatcaataggaagaagggtgcca 660  
Qy 900 ccattcgaacatcaccaaacagaccagctcaaaatcgatgtccaccgttaaaagaagaatg 959  
Db 661 ccaatcggaaacatcaccaaacagaccagctcaaaatcgatgtccaccgttaaaagaagaatg 720  
Qy 960 cgggggctgctgagaagtcgattactatcctctactcctctactcctgaaggcacctctgcgctt 1019  
Db 721 caggggctgctgagaagtcgattactatcctctactcctctactcctgaaggcacctctgcgctt 780

Qy 1020 gtaagtctattctggagattatgcataaaggagctcaagatatataaaattcacagaaga 1079  
Db 781 gtaagtctattctggagattatgcataaaggagctcaagatatataaaattcacagaaga 840  
Qy 1080 tcccttgaagatttttagctcataataaactttgttgacgtctctatttgtaaaagaagaa 1139  
Db 841 tcccttgaagatttttagctcataataaactttgttgacgtctctatttgtaaaagaagaa 900  
Qy 1140 gaaatcttaaaaaaattigacagacacagacactaaatcacgatattcctcattgcagg 1199  
Db 901 gaaatcttaaaaaaattigacagacacagacactaaatcacgatattcctcattgcagg 960  
Qy 1200 aattgacgtgtataatccagaaacgcctattacagtttaaaggcgaattgttgagacatgt 1259  
Db 961 aactgatgcagataaattccagaaacacacacctatcacgtctaaaggcgaattgtgagacatgt 1020  
Qy 1260 ccaagctggaggagagatcatgaagaaatcaggggagctcttgaataatgatattgctt 1319  
Db 1021 ccaagctggaggagagatcatgaagaaatcaggggagctcttgaataatgatattgctt 1080  
Qy 1320 ctatgaactctcaagcacatttaattccttgatttaaatctgaacgccttgggtctgttcc 1379  
Db 1081 ctatga--tttcaagcacatttaattccttgatttaaatctgaacgccttgggtctgttcc 1138  
Qy 1380 caccacttcagggtatgccactcccactcagggccccccttcaggccatgactcctcct 1439  
Db 1139 caccacttcagggtatgccactcccactcagggccccccttcaggccatgactcctcct 1198  
Qy 1440 acccgagtttgagcaatcagaaacggagactgttcatcagtttatccagctctatacag 1499  
Db 1199 cccgcgactgtgagcaatcagaaatcccgactgttcatctgtttatcccgctctacag 1258  
Qy 1500 tcggtgcactcatcgcaagcagggccagcacatcaagcagcttctcgccttgcgtcagag 1559  
Db 1259 tcagagccctcatcagcaagcagggccagcacatcaagcagcttctcgccttgcgtcagag 1318  
Qy 1560 cttaaatgaagattgtccagcggaagcaccagatgctaaagtgaggtggtgattatca 1619  
Db 1319 cttaaatgaagattgtccagcggaagcaccagatgctaaagtgaggtggtgattatca 1378  
Qy 1620 ctggaccacacagaggtcagttcaagctcagggagaatttatggaaaaataaagaag 1679  
Db 1379 ctggaccacacagaggtcagttcaagctcagggagaatttatggaaaaataaagaag 1438  
Qy 1680 aaaaactttagtccctaaagaaggtgaaacttgaagctcatatcagagtgccactct 1739  
Db 1439 aaaaactttagtccctaaagaaggtgaaacttgaagctcatatcagagtgccactct 1498  
Qy 1740 ttgctgtgagaggttattggaaaaaggaggaacacgggtgaaatgaaacttcagaaattgt 1799  
Db 1499 ttgctgtgagaggttattggaaaaaggaggaacacgggtgaaatgaaacttcagaaattgt 1558  
Qy 1800 caagtgcagaagttgttccctcgtgacacagacacactgatgagaatgaccaagtgttg 1859  
Db 1559 caagtgcagaagttgttccctcgtgacacagacacactgatgagaatgaccaagtgttg 1618  
Qy 1860 tcaaaaataactgttccacttctatgttgcaggttgcacagagaaaaatccaggaaattc 1919  
Db 1619 tcaaaaataactgttccacttctatgttgcaggttgcacagagaaaaatccaggaaattc 1678  
Qy 1920 tgactcgggttaagcagcaccaacacagaaggtcctgcgaagtggaccacctcagtcacaa 1979  
Db 1679 tgactcgggttaagcagcaccaacacagaaggtcctgcgaagtggaccacctcagtcacaa 1738  
Qy 1980 gacggaagttaaggctcagaaacagcccacacagagggcagatgccaaaccaaagcag 2039  
Db 1739 gacggaagttaaggctcagaaacagcccacacagagggcagatgccaaaccaaagcag 1798  
Qy 2040 atgtcttaacaaacagatggcgctgacccctctatccagaaatcacatgcacaaagtttta 2099  
Db 1799 atgtcttaacaaacagatggcgctgacccctctatccagaaatcacatgcacaaagtttta 1858

QY 2100 cctagccagttgttcttgaggaccaggaactttttgaact-cctgtctctctgtggaagt 2159  
|||||  
Db 1859 cctagccagttgttcttgaggaccaggaactttttgaactcctgtctctgtggaagt 1918  
|||||  
QY 2159 atactttatgctctgtaaatgtatgacaccagcttttaaacacaaacaaacaaaca 2218  
|||||  
Db 1919 atactttatgctctgtaaatgtatgacaccagcttttaaacacaaacaaacaaaca 1978  
|||||  
QY 2219 aaaaaag 2225  
|||||  
Db 1979 aaaaaag 1985  
|||||

## RESULT 4

PCT-US01-08631-6785  
; Sequence 6785, Application PC/TUS0108631  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-049  
; CURRENT APPLICATION NUMBER: PCT/US01/08631  
; PRIORITY FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO 6785  
; LENGTH: 2010  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIMILAR  
; LOCATION: (50)..(1843)  
; OTHER INFORMATION: 100% homologous to Homo sapiens IGF-II mRNA-binding protein  
; OTHER INFORMATION: 2, accession number AF117107, Smith-Waterman Score=3059.  
PCT-US01-08631-6785

Query Match 17.0%; Score 710.4; DB 1; Length 2010;  
Best Local Similarity 64.5%; Pred. No. 1.2e-129;  
Matches 1155; Conservative 0; Mismatches 556; Indels 81; Gaps 3;

QY 251 atgaacaaactgtatatcggaacactcagcagagaacgcgcgccttcgacactagaaagt 310  
|||||  
Db 50 atgaacaaactgtatatcggaacactcagcagagaacgcgcgccttcgacactcgcgcgag 109  
|||||  
QY 311 atcttcaaggacgcgaagatcccggtgtctcggaaccccttcctgtgtgaagactggtacgcg 370  
|||||  
Db 110 ctcttgggacagagaagctgccttcggtggacagagctcctgtgtaagtcccggtacgcg 169  
|||||  
QY 371 tctgtgactcgcgcgacagagactggccctcaaggccatcgagcgcgttccttcaggtaaa 430  
|||||  
Db 170 tctgtgactcgcgcgacagagactggccctcaaggccatcgagcgcgttccttcaggtaaa 229  
|||||  
QY 431 atagaactcgcgcggaaccccaatagaagtgtgacactcgttcgcccacaaaggcaagatt 490  
|||||  
Db 230 gfggaattgcatgggaacatcaggaattgattactcagctctctaaaggctaaaggagc 289  
|||||  
QY 491 cggaaactcagatcagaaataatccgcctcatttacagtgaggaggtgctggaatttta 550  
|||||  
Db 290 aggaataatcagatcgaacatacctcctcctcagctgcagtgagggtgttgatggactt 349  
|||||  
QY 551 ctagtccagatgagtggtgagagcgtgtgagcaagtgaacactgactcggaaactgca 610  
|||||  
Db 350 tgggtcctaattgagacagtggaagtgtggaacagtcacacagacacagaaacccgc 409  
|||||  
QY 611 gttgtaaatgtaacctattccagtaggaaccaagcttagacaagcactagacaaactgaat 670  
|||||  
Db 410 gttgcaacgtcacataigcaacaagagaagacaaataagcattgagagactaagc 469  
|||||  
QY 671 ggaattcagttagagaatttcaccttgaaagttagcctatatcctcctgatgaaatggccgc 730  
|||||

Db 470 gggaatcagtttgagaactactccttcaagatttctcatctccatcccgatgaagtgagc 529  
|||||  
QY 731 cagaaaaaccccttcagcagcccgaggtgcgcggggttggcagaggggctccctca 790  
|||||  
Db 530 tcccttcgccccctcagcagcccgagcgtggggaccactcttccgggagcaaggccac 589  
|||||  
QY 791 aggcaggggttccaggtacogtatcccaagcagaacacctgtgatttccctcgcgcgtg 850  
|||||  
Db 590 g-----cccttggggcacttctcagccagacagattgattcccgctcggaac 640  
|||||  
QY 851 ctggttcccaacccaaattgttgagccatcatagaaagaaggtgccaccatttcggaac 910  
|||||  
Db 641 ctggttcccaacccaaattgttgagccatcatcgaaaggagggcttgaccataaagaac 700  
|||||  
QY 911 atcacaacacagaccagctctaaatcagatgccaccgttaaagaaaaatgcgggctgct 970  
|||||  
Db 701 atcactaagcagaccagctcccggttagatataccatagaaaagagaactcttgagctga 760  
|||||  
QY 971 gagaagtcgattactctctctactctgaagcactctgcggcttgcgttgaagtctatt 1030  
|||||  
Db 761 gagaagcctgtccaccatccatgcaccaccagagggactctgaagcatgccgcgcatgatt 820  
|||||  
QY 1031 ctggagattatgcataaagaagctcaagatatataaattcacagaagagatcccttgaag 1090  
|||||  
Db 821 ctggaatcatgcagaagaagcagatgagaccaaactagccgaagagagattctctctgaaa 880  
|||||  
QY 1091 attttagctcataataactttgttgagcgtcttattgttaaagaaggaagaactcttaaa 1150  
|||||  
Db 881 atcttggcacaaatggcttggtagagactgattgaaagaaggaggaatattgag 940  
|||||  
QY 1151 aaaaattgagcagacacagacactaaatcacgatatctccattgcagaaattgcgcgtg 1210  
|||||  
Db 941 aaaaattgacatgaacagggccaagataaacaatctcatcttgcagatttgagcata 1000  
|||||  
QY 1211 tataatcagaacgcactattacagttaaagcaatgttgagacatgtgtcccaaaagctgag 1270  
|||||  
Db 1001 tacaacccggaaagaaacatcactgtgaaggcagctgtgagcctgtgccagtgctgag 1060  
|||||  
QY 1271 gaggagatcatgaagaaaaatcaggagcttattatgaaatgatatgtctctatgaatt 1330  
|||||  
Db 1061 atagagattatgaagaagcgtgcgtgagccttgaagaatgatatgctggtttaaaca 1120  
|||||  
QY 1331 caagcacatttaattctcgtgattaaatcgaacgccttgggtctgttcccccacttca 1390  
|||||  
Db 1121 caagcacaattctgattcccgaggttgaaacctcagcagcttgcatcttttcaacagagctg 1180  
|||||  
QY 1391 gggatgccactcccaacctcaggggcccttcagccatgactcct----- 1435  
|||||  
Db 1181 tccgtgctatctccaccagcaggcccgcgagctcccccgctgcccccctaccaccc 1240  
|||||  
QY 1436 -----ccctaccgcagtttgagc----- 1454  
|||||  
Db 1241 ttcaatccccactccggataacttctccagctgtaccoccatcaccagtttggcccgcttc 1300  
|||||  
QY 1455 -----aatcagaacggagactgttcactagtttatccagctctatca 1498  
|||||  
Db 1301 ccgcatcatcactcttaccagagcagagattggaactctcttcatcccaacacagct 1360  
|||||  
QY 1499 gtcgtgccaatcatcggcaagcagggccacacatacgaagcagcttctcgttctgtgga 1558  
|||||  
Db 1361 gtyggcgccaatcatcgggaagagggggcacacatacgaagcagctggcgagattcgccgga 1420  
|||||  
QY 1559 gcttcaattaaagatgctccagcggaaagcaccagatgctaaagtaggaggtggtatc 1618  
|||||  
Db 1421 gctctataagattgccccctcggaagccacagcgtcagcgaaggaggtggtcatc 1480  
|||||  
QY 1619 actgaccacagaggtcagttcaaggctcaggggaagaatttatggaaaaataaagaa 1678  
|||||  
Db 1481 accggccacccggaagcccgagttcaaggcccgagcagcttcttgggaactgaaagag 1540  
|||||  
QY 1679 gaaaactttgttagtctcaagaagagggtgaaacttgaaagctcaatcagatggcacc 1738  
|||||

Db	1541	gaaaactctttaacccccaaagaagaagtgaagctggaagcgcataatcagatgcccctct	1600
Qy	1739	tttgctgctggcagagattattgaaagaaagagcgaacacggtgaatgaacttcagaatttg	1798
Db	1601	tccacagctggccgggtgatgtgcgaaggtaggaagaccgtgaaacgaactgcagaactta	1660
Qy	1799	tcaagctgcagaagttgtttctccctcgttcaccacagacacactgtatgagaatgccaaagtgttt	1858
Db	1661	accagctgcagaagtcactgctcgttcaccacacgcagatgaaatgggaagtgtac	1720
Qy	1859	gtcaaaataactgtgtcaactcttatctgttcgcaggtgtccacagagaaaaattcaggaaatt	1918
Db	1721	gtcagaattatcgggcacactctttctctagcagactgcacagtcgaagatcaggggaaatt	1780
Qy	1919	ctgactcaggttaagcagcaccacaaacagaaggtctgtcaaatgggaccac	1970
Db	1781	gtacaacagttgaagcagcagagcagagaaataccctcaggaagtgcgctcac	1832

## RESULT 5

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PCT-US01-08631-6786
; Sequence 6786, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 6786
; LENGTH: 3667
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (436)..(2103)
; OTHER INFORMATION: 100% homologous to Homo sapiens hepatocellular carcinoma
; OTHER INFORMATION: autoantigen,accession number AF057352,Smith-Waterman Score=2838.
PCT-US01-08631-6786

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Query Match	16.6%	Score 695.6	DB 1	Length 3667
Best Local Similarity	64.8%	Pred. No. 1e-126		
Matches 1115; Conservative		0; Mismatches 539	Indels 66	Gaps 3

Qy	251	atgaacaaactgtatatcggaacctcagcagaacgcgccccttcggacctgaaaagt	310
Db	439	atgaacaagctttacattcgggaaccttgaccgccgctcaaccgcgcagacctccggcag	498
Qy	311	atcttcaaggacccaagatccccggtgtcgggaccttctctggttaagaactgctacgcg	370
Db	499	ctctttggggacagaagctgccctcggcgacaggtcctctgaagtcocggtcacgcc	558
Qy	371	ttcgtggactgcccgacgacgagactggcgccctcaaggcccatcgagcgttttcaggtaaa	430
Db	559	tctgtggactaccgccacgacgactggggccataccgcgccatcgagacctctcgggttaa	618
Qy	431	atagaactgcacgggaaacccatagagttgtagcactcgtgccaaaaaggcaaggatt	490
Db	619	gtggaaattgcattggaaaatcatggaattgatattactcagttctctaaaagctaaggac	678
Qy	491	cggaaacttcagatatacgaataatcccgccctcatttacagttgggagtgctggatgttta	550
Db	679	aggaaaattccagattcgaaacatccctcctcacttcagttgggaggtgttgatggactt	738
Qy	551	ctagttccagtatggagtgttgagagacttgtgaccaagtgaacactgactctcggaactgca	610
Db	739	ttyggtccaatatgggacagtgtggagaattctgggaacaagttcaacacagacagaaaccgcc	798











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; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 12584
; LENGTH: 1998
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (3)..(1469)
; OTHER INFORMATION: 31% homologous to Herpesvirus papio NTR, accession number
; OTHER INFORMATION: AF200364, Smith-Waterman Score=247.
PCT-US01-08631-12584

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Query Match      4.1%; Score 170.2; DB 1; Length 1998;
Best Local Similarity 98.3%; Pred. No. 2.9e-24;
Matches 172; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1811 gttgttgcctcgtgaccagacacctgatgagaatgaccagtggtgttgcataataact 1870
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 462 ggtgttgcctcgtgaccagacacctgatgagaatgaccagtggtgttgcataataact 521

QY 1871 ggtcacttctatgcttgcaggttgcacagagagaaaaattcaggaaaattctgactcaggtta 1930
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 522 ggtcacttctatgcttgcaggttgcacagagagaaaaattcaggaaaattctgactcaggtta 581

QY 1931 aagcagcaccacaacagagaggtctgtgcaagtggaccacctcagtcacagcagga 1985
      ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 582 aagcagcagcaacacagaggtctgtgcaagtggaccacctcagtcacagcagga 636

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Search completed: September 29, 2001, 10:05:25  
Job time: 10768 sec

